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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
          Copyright
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- protein search, using sw model OM protein

2004, 02:20:31; October 23, Run on:

; Search time 108 Seconds (without alignments) 2019.139 Million cell updates/sec

US-10-007-527A-2 2005 1 MISVSABHLSGKDRPPVLVS........HLHYRLPAADVRPPIISVRK 379 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O84bc5 rhodococcus				. 4	_	-	Aas03171 mycobacte	Q8sch7 propionibac	Q9x3u7 bifidobacte	Q8ggd7 streptomyce													strepton	Q84ge5 corynebacte	O69069 streptomyce	Q45282 corvnebacte				Q56129 streptococc
SUMMARIES	ID	Q84BC5	P94171	Q8GDF1	069764	Q84GF4	Q9RIQ0	Q742I1	AAS03171	Q8SCH7	Q9X3U7	Q8GGD7	QBRIU6	Q93L41	Q9R881	REP STRLI	Q8GHF1	Q9AGT3	Q52220	Q57477	QBRNS3	083016	Q54245		NEOR_STRCY	Q84GE5	690690	Q45282	Q84FM7	086156	REP LACHI	Q56 <u>1</u> 29
	DB	2	7	~	7	7	7	~	~	~	N	~	N	7	N	Н	7	7	~	7	~		7									
	Length	379	459	433	403	482	476	525	525	405	380	622	471	461	401	456	312	396	396	528	478	202	481	437	437	389	396	240	313	261	314	315
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	Score	2005	609.5	269	497	425.5	424.5	409	409	374.5	373	360.5	345	342.5	326	316	315.5	293.5	277.5	266.5	N	256.5	235.5	230.5	N	214.5	194	Ð	163.5	•	12	123.5
	Result No.	н	7	m	4	Ŋ,	9	7	00 (יים	0 7	7,	12	13	14	12	16	17	18	19	20	21	22	523	4, T	52	910	7.7	28	53	30	31

Obdrr7 strentococc	0842e5 strentococc						070ld8 streptococc	Cad97600 strentoco	09x9n4 streptococc	O30850 strentococc				
Q6DRR7	O842E5	O9RNV8	O9RNW4	OPRIVES	O9ZNC0	006460	070LG8	CAD97600	Q9X9N4	030850	Q9K4S9	052769	052776	
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334	315	315	315	315	319	336	311	311	315	314	276	320	320	
6.1	6.1	6.1	6.1	6.1	5.9	5.7	5.7	5.7	5.7	5.7	9.6	5.6	9.6	
123	122.5	122.5	122.5	121.5	119	115	114.5	114.5	114.5	114	111.5	111.5	111.5	
32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQALELWREFEFGSMGRRAIAWSRGLRARA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MISVSAEHLSGKDRPPVLVSSDKRGIRHELRPKLQQITTSETFNACGRPISGVNGVTIVN 60
                                                                                                                                                                                                                                                                  Rhodococcus erythropolis.

Rhodococcus erythropolis.

Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Nocardiaceae; Rhodococcus.

XX (UBL_TaxID=1833;

XI (1)

SEQUENCE FROM N.A.

REDIAND=22718480; PubMed=12835922;

XI ROBLIND=22718480; PubMed=12835922;

XI A small cryptic plasmid from Rhodococcus erythropolis:

Characterization and utility for gene expression.";

XI Appl. Microbiol. Biotechnol. 62:61-68(2003).

REDIAND=277; ANO31602.1;

XI Appl. Microbiol. Biotechnol. 62:61-68(2003).

REDIAND=277; PubM binding; IEA.

RO; GO:0005727; C:extrachromosomal circular DNA; IEA.

RO; GO:000560; P:DNA replication; IEA.

RICEPPO: IPRO00999; Rep.

REPIN: PF001446; Rep_1: 1.
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                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2005; DB 2;
Pred. No. 1.8e-152;
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100.0%; Pred. No. ...
0; Mismatches
                                                                  379 AA
                                                                  PRT;
                                                                                                                          (TrEMBLrel. 24, (TrEMBLrel. 24, 1) (TrEMBLrel. 26, 1
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Matches 379; Conservative
                                                                                                                    (Tremblrel. (Tremblrel.
                                                              PRELIMINARY;
                                                                                                                                                                                                                  Replication protein.
                                                                                                                    01-JUN-2003
01-JUN-2003
01-MAR-2004
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                                                              Q84BC5
Q84BC5;
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RESULT 1
Q84BC5
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RRAIAWSRGLRARAGLGAELTDAQIVEQEESAPVMVAIIPARSWMMIRTC-APYVFGEI- 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGKGWICPCCAGKVGAHRADEISQVVAHQLGTG-SVAMVTMTMRHTAGQRLHDLWTGLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 CGSVWACPVCAAKISAHRRDELARVVQVAVGLGFRVSMLTLTQRHHAGQDLAELWASLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 RKQGRRTTPYPEEVQRPEDFIAERWSRGLRKRGVDFIA---GSGGLDWQTADSGDEEALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 AYLTKIAS---GVGMEVGSGDGKSGRHGNRAPWEIAVDAVG-GDPQALELWREFEFGSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 PVLVSSDKRGIRHELRPKLQ--QITTSETFNACGR-PISGVNGVTIVNGPKGSGFGGLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNGWHVHVHVHALLMFSGD----VSENI---
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                        Propionibacterium granulosum.
Plasmid cryptic plasmid pPG01.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                        STRAIN=PF283;
Farrar M.D., Holland K.T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databages.
EMBL; AX150274; AAN78123.1; -.
GO; GO:000577; C:extrachromosomal circular DNA; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006560; P:DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA; 48340 MW; 1A8C34C0FBF8678F CRC64;
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annotation update)
                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

28.4%; Score 569; DB 2;
Best Local Similarity 35.6%; Pred. No. 3.5e-37;
Matches 136; Conservative 63; Mismatches 145.
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                           PRT;
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                                                         (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 26, I
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01-AUG-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                            PRELIMINARY;
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Plasmid.
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=33011;
                                                                          01-MAR-2003
01-MAR-2004
                                                             01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-----DVRKIGGEADQVLAAYLTKI----ASGVGMEVGSGDGKSGRHGNRAPWEIAVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEHLSGKDRPPVLVSSD-----KRGIRHELRPKLQQITTSETFNACGR-PISGVNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 TIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTG-SVAMVTMTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 MFSGDVSENILESF------SDAMFDRWTSKLVSLGFAAPLRNSGG
GLGAELTDAQIVEQEESAPVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDH
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98292760; PubMed=9620977;
MEDLINE=98292760; PubMed=9620977;
Billington S.J., Jost B.H., Songer J.G.;

Dillington S.J., Jost B.H., Songer J.G.;

of the plJ101/pJV1 family of rolling circle replication plasmids.";

J. Bacteriol. 180.333.3336(1998).

GO; GO:0005727; C:extrachromosomal circular DNA; IEA.

GO; GO:0005277; E:DNA binding; IEA.

InterPro; IPR000989; Rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARSWAMIRICAPYVFG--EILGLVEAGA----TWENLRDHLHYRLP 366
                                                                                                                                                                                                                                                                                                                         Pidamiu presidenta, Actinobacteria, Actinobacteridae, Actinomycetales, Actinomycineae, Actinomycetaceae, Arcanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 609.5; DB 2; Length
; Pred. No. 2.1e-40;
62; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA; 51264 MW; 2A0A4B0A043BF865 CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                 459 AA
                                                                                                                                                                                                                   Created)
                                                                                                                                                                                 PRT;
                                                                                      LHYRLPAADVRPPIISVRK 379
                                                                  LHYRLPAADVRPPIISVRK 379
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il Similarity 36.3%;
148; Conservative 6
                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                               Arcanobacterium pyogenes.
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01446; Rep_1; 1
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                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1661;
                                                                                                                                                                                                                                                                                                               Plasmid pAP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 SDRKQRGVSVNPVVERGISLMTLTLRHNSKQSLTEVWDAIAGGWQAVINTAAWRGGARTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 TEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGDVSENILESFSDAMFDRWISKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 LGFAAPLRNSGGLDVRKIGGEADQV--LAAYLTK-IASGVGMEVGSGD-GKSGRHGNRAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GPKG-SGFGGLRSCGKGWICPCCAGKVGAHRADEISQVV-------AHOLGTGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VAMVIMIMRHTAGQRLHDLWIGLSAAWKAAINGRRWR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 LGMRAPSRDR-GIDVVHVAASSDDAKSIGGYTCKGMLSGIAAETTTGQVTKEAKGDNRTP
                                                                                                                                                                                                                                                               2; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=68242;
                                                                                                                                                                                                                                                                                                                                              Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ243257; CAB62261.1;
GO; GO:0005727; CEXTRACTYCOMOSOMAL Circular DNA; IEA.
GO; GO:0005677; F.DNA binding; IEA.
GO; GO:0006260; P.DNA replication; IEA.
                                                                                                                                                                           482 AA; 52145 MW; F5D493A32F5C7F6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                  21.2%; Score 425.5; DB 2; 29.1%; Pred. No. 1.3e-25; ative 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.2%; Score 424.5; DB 2; Best Local Similarity 29.7%; Pred. No. 1.5e-25; Matches 121; Conservative 53; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 AA.
            GO, GO:0006260; P:DNA replication; IEA InterPro; IPR000989; Rep. Pfam; PF01446; Rep_1; 1. Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                      Matches 109; Conservative
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Plasmid,
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                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDRWISKLVSLGFAAPLRNSGGLDVRKIGGEAD-QVLAAYLIK--IASGVGMEVGSGDGK 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGRH--GNRAPWEIAVDAVGGDPQALELWREFEFGSMGRRAIAWSRGLRARAGLGAELTD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 AQIVEQE-ESAPVMVAIIPARSWM-------MIRICAPYVFGEILGLVEAG-ATWEN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Propionibacterineae; Propionibacteriaceae; Propionibacterium.
NCBI_TaxID=1744;
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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"Plasmids in Corynebacterium glutamicum and their molecular classification by comparative genomics.";
"Biotechnol. 104:27-40(2003).
EMBL; A112664; AA018194.1:
GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%; Score 497; DB 2; Length 40. 34.0%; Pred. No. 2e-31; ive 63; Mismatches 144; Indels
                                                                                            SEQUENCE FROM N.A.

Dasen G.H., Miescher S., Teuber M., Meile L.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

BBL; AJ006662; CAA07175.1; -.

GO; GO:000577; C:extrachromosomal circular DNA; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO: GO:0006260; P:DNA replication; IEA.

InterPro; IPR000989; Rep.

Pfam; PF01446; Rep_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 AA; 43502 MW; 340F40AA697E880C CRC64;
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Last sequence update)
Last annotation update)
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MEDLINE=22830013; PubMed=12948627;
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LQEHGIEHELVEVD 403
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Matches 127; Conservative
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SEQUENCE Query Match

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                                                                                                37 ITTSETFNACGRPISGVNGVTIVNGPKGSGF-GGLRSCGKGWICPCCAGKVGAHRADEIS
                                                        85; Gaps
                            Length 476;
                                                      Indels
476 AA; 51890 MW; DEE4C8B3CC2B5B95 CRC64;
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REFERGSMGRRAIAWSR-------GLRARAGLGAELTDAQIVEQEESAPVMVA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 BRRRIRWGARAMLWQASSLKAVRCCGRVLHNDAVGDPDG-QGVVIKRREVDGRMVASLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 LGGHGWHLHIHALVFSVTSLSSGLIEGIERTLGRGVNHDWLARNVFAARIHQRWSQGLAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 NOTPFEVLANLAESVDARGFGIRTPRHWAVLPAGNGDWAVIDSDTGEVASITAPGQWKVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 DKRGIRHELRPKLQQITTSETFNACGR-----PISGVNGVTI----VNGPKGSGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRSCGKGWICPCCAGKVGAHRADEISQVV--AHQLGTGSVAMVTMTMRHTAGQRLHDLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- POALELW
                                                                                                                         416 HEWEQASCGRROITWSRRRSNPESGREMLWNDLLDSRGRSAEASDEEIAVDEVDAE-SVG
-- POALELW
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128;
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017229; AAS03171.1; -.
Hypothetical protein.
SEQUENCE 525 AA; 56735 MW; DDBSEB33E6BD35FD4 CRC64;
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Hypothetical protein.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                              525 AA
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                                                                                                                                                                                                    IIPARSWMMIRTCAPYVFGEILGLVEA 350
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      NRAPWEI -----AVDAVG
                                                                                       278 REFEFGSMGRRAIAWSR-
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02-MAR-2004
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                                                                                                                                       SRHTLAELVIQQRDAWKKALGQNAGRDWRKAKKDYGVVGFVRAWEVIYGEANGWHPHWHV 179
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                                                                     AAGTAWEDIGGINGPKIRPARAAWKKDINDRTAEDWAAIBEADGLQAGGLGMLTLTMRHY
                                                                                                                                                                                                      LLMFSGDVSENILESFSDAMFDRWTSKLVSLGFAAPLRNSG-GLDVRKIGGEADQVLAAY
                                                                                                                                                                                                                                 LIKIASG-----VGMEVGSGDGKSGRHGNRAPWEIA-----VDAVGGD-PQALELWREFE
                                                                                                                                                                                                                                                                                                                                                                                                                      298 TAARGMRALYWSNGLRKRLAALVELDTRTDGEIAAEERQGEALAVILADPWHQHIARRKG
                             -- VAHQLGTGSVAMVTMTMRHT
                                                                                                                   AGQRIHDIWTGLSAAWKAATN---GRRWRTEREMYGCDGYVRAVEITHGK-NGWHVHVHA
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                                                                                                                                                                                                                                                                                                                                                                             FGSMGRRAIAWSRGLRARAGLGAEL---TDAQIVEQEESAPVMVAII-----
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AE017229; AAS03171.1; -.
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SEQUENCE 525 AA; 56735 MW; DDB5E83E68D35FD4 CRC64;
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OrderedLocusNames=MAP0854;
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 AGORLHDLWTGLSAAWKAATINGRRWRTEREMYGCDG---YVRAVEITHGKNGWHVHVHAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G----SGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVA--HQLGTGSVAMVTMTMRHT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: : : | : | : | : | 185 VLLGEGARGREADAVEQIRARMGSWNRAVVRQGLKSGLESLSEAHLIEPDAGDGLGGLA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 WREFEFGSMGRRAIAWSRGLRARAGLGAELT--DAQIVEQEESAPVMVAIIPARSWMMIR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLSGKDRPPVLVSSDKRGIRHELRPKLQQITTSETFNACGR-PISGVNGVTIV---NGPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GNVIDAGYSGLQHCNSVWACPVCAAQIASQRQMLVSEVLSRWHARG-GRAMMITLIVRHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 LMFSGDV---SENILESFSDAMFDRWTSKLVSLGFAAPLRN-SGGLDVRKIGGEADQVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 HADGSNR-----RRRVRWSARRILWIGSGLORVRNCGRVPRSLSSGVAIMVRRDSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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Bifidobacteriaceae, Bifidobacterium.
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MEDLINE=99271179; PubMed=10339821;
O'Riordan K., Fitzgerald G.F.;
"Molecular characterisation of a 5.75-kb cryptic plasmid from
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 405;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21886396; PubMed=11889111;
Chopin M.C., Rouault A., Ehrlich S.D., Gautier M.;
Filamentous phage active on the gram-positive bacterium
Fropionibacterium freudenreichii.";
J. Bacteriol. 184:2030-2033 (2002).
EMBL, AF42826; AAL91702.1;
SEQUENCE 405 AA; 44762 MW; D84BSEC4819D4F90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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18.7%; Score 374.5; DB 2;
Best Local Similarity 29.4%; Pred. No. 1.3e-21;
Matches 111; Conservative 62; Mismatches 154;
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                                                                                                                          Propionibacterium phage phiB5.
Viruses; ssDNA viruses; Inoviridae; Inovirus
NCBI_TaxID=189836;
               405
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             PRT;
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           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Plasmid pCIBb1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
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                                                                                                                                                                                                                                                                                                                                                                                                                          -------GTGSVAMVTMTMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTEREMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 KKDGNPYNVAP-NDEHGIDLQFKSGKDAGTAAAEYITKIQGDKGGVTLAQEIARGDIKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 RHGNRAPWEIAVDAVGG--DPQALELWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 EGQRLPPELMVSDSFGNYIFGTLTLRHDRTMPLAMTLDAILKGWTKMINGSPWQRASERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GCDGYVRAVEITHGKNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTS--KLVSLGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AAPLRNSGGLDVR-KIGGEADQVLAAYLTKIASGVG-----MEVGSGDGKSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coombs J.T., Franco C.M.M., Loria R.; "Complete sequencing and analysis of pEN2701, a novel 13-kb plasmid from an endophytic Streptomyces sp."; Plasmid 49:86-92(2003).
                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                             58 IVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 IVEQEESAPVMVA-IIPARSWMMIRTCAPYVFGEILGLVEAGATWENL 357
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                                                                                                                                                                                                                                                                                                    Length 380;
       mode
                                                                                                                                                                                                                                           380 AA; 42758 MW; D26F597563E604FA CRC64;
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Last sequence update)
Last annotation update)
Bifidobacterium breve NCFB 2258 and determination
                                                                                                                                                                                                                                                                                            18.6%; Score 373; DB 2; L 27.9%; Pred. No. 1.6e-21; ive 56; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycetaceae; Streptomyces.
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18.0%; Score 360.5; DB 2;
Best Local Similarity 24.5%; Pred. No. 2.8e-20;
Matches 113; Conservative 56; Mismatches 155;
                                                                                            GO; GO:0005727; C:extrachromosomal circular GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR000989; Rep.
Pfam; PF01446; Rep_1; 1.
                       replication.";
FEMS Microbiol. Lett. 174:285-294(1999)
EMBL; AF085719; AAD34709.1;
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Plasmid.
                                                                                                                                                                                                                                                                                                                                             97; Conservative
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                                                                                                                                                                                                                                                                                                                      Local Similarity
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NCBI_TaxID=211464;
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260 WEIAVDAVGGDPQALE-----LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQIV- 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----WAELCDDVHKRLDI 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAHRADEISQVVA--HQL-GTGSVAMVIMIMRHTAGQRLHDLWTGLSAAWKAATNGRRWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 TEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 IGFAAPLRNSGGLDVRKIGGEADQV-LAAYLTK-IAS--GVGMEVGSGDGKSGRHGNRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 HGWQRPSWEH-GIDLVQSTGRDDAIMMGAYTAKGIAESWNAASEVAGQAFKEAKGTNRTP
                                                                                       GDPOALELWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQIVEQEESAPVMVAIIPAR
                                         240 VAAFEAHAIDVKGWCTASDYLAKODDSRHWGVDAEIAKASTKAGRAKGKHPFALLTLFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 15991;
Venkova T., Patek M., Nesvera J.;
Venkova T., Patek M., Nesvera J.;
Venkova T., Patek M., Nesvera J.;
Characterization of the cryptic plasmid pCC1 from Corynebacterium callunae and its use for vector construction.";
Plasmid 51:54-60(2004).

EMBL; AJ308231; CAC59945.1; -.
GO; GO:0005272; G:extrachromosomal circular DNA; IEA.
GO; GO:0005260; P:DNA binding; IEA.
GO; GO:0006260; P:DNA binding; IEA.
InterPro; IPR000989; Rep.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Mismatches 163;
                                                                                                                                                                                                         359 OWKLIRQAG--LRAKVLDLAESNGGWVAIQ-HL 388
                                                                                                                                                                              SWMMIRTCAPYVFGEILGLVEAGATWENLRDHL 361
                                                                                                                                                                                                                                                                                                                                     461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative replication initiation protein
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GEVLGEDEATEDYVVADIPAKA----
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01-DEC-2001 (TEMBLrel. 19, Last seq
01-MAR-2004 (TEMBLrel. 26, Last ann
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Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium callunae
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Plasmid.
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      22B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 HVHVHAHLIMFSGDVSENILESFSDAMFDRWTSKLVSLGFAAPLRNSGGLDVRKIGGEADQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPHTHELWFVDAGTDADTMKK---TVLERWKTSCARAGL-----LDL----DNADQ 239
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         -TAGQ----- 120
                                    :: | | | | : : | | | | OARIRAARAVELERAALAWLKAGHGIYMATITVPHWEHVRLAASRVKDGHKCAGQRSCTCP 124
                                                                                                                                                                                                                                                                                                   245 SHAHVLIWTEDEATDARAERIEEELYNRWAKRCKAVGLPTPARGEIRPKDGKRIGKGVDV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQIVEQEESAPVMVAIIPARSWMMIR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTG-SV
                                                                                                                         TAVDRIALETDGRYVRRQEFGPDGRPSGPATVWQEGFRDRWGIVGTTRTIEITWGANGWH
                                                                                                                                                                                                                                                                                                                                                                                          TAATREKAGAVGKYVIKLQEGGNLAMEMTRADLKVARGQKGKTA-LELAAVAASGNEQAL
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                                                                                                                                                                                                                                                                         169 VHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSLGFAAPLRN-----SGGLDV
                                                                                                                                                                                                                                                                                                                                                            RKIGGEADQVLAAYLTKIASG--VGMEVGSGDGK--SGRHGNRAPWEIAVDAVGGDPQAL
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

NCBI_TaxID=47880;
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26.7%; Pred. No. 3.6e-19;
ive 57; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh N., Kawanami T., Nitta C., Iwata N., Usami S., Abe Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000989; Rep.
Pfam, PF01446; Rep I; 1.
SEQUENCE 471 AA; 51989 MW; C4443E8BEFFE1941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 TCAPYVFGEILGLVEAGATWENLRDHLHYRLPAADVRPPII 375
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Last annotation update)
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           AGKVGAHRADEISQVVAHQLGTG-SVAMVTMTMRH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical Rep protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Conservative
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Best Local S
Matches 89
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QRIUG
1D QRIUG
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DT 01-JU
DE HYPOT
GN Name=
OS PSEUC
OC PSEUC
OC PSEUC
OC STAN
EN [1]
RP [1]
RP STAN
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DR G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNDAPLREHGVKLDQVSTWGGDAAK-MATYLAK---GMSQELTGSATKTASKGSYTPPQM 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMYGCDGYVRAVEITHG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFAAPLRNSG-GLD-VRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPWEI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVDAVGGDPQALE-----LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQI--- 311
                                                                                                                                                                                                                                                                                                                                                                                                          34 LQQITTSETFNACGR-----PISGVNGVIIVNGPKGSGFGGLRSCGKGWICPCCAGKV
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MYKITINSKALAGCHRWRRDEAVAVSWSS-----NG--ASQFEGLQNSHSRWGSPLAELEV
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINS-ATC 21086;
MEDLINE-96276208; PubMed-8693028;
Ankri S., Reyes O., Leblon G.;
"Electrotransformation of highly DNA-restrictive corynebacteria with
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinee; Corynebacterinee; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                         58; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                 Ankri S., Reyes O., Leblon G.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092037; AAD08690.1; -.
                                                                                                                                                                                                                                                                    Reyes O.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                     401 AA; 44481 MW; 5E0590D936132C4D CRC64;
                                                                                 Last sequence update)
Last annotation update)
                                                                                                                     Corymebacterium glutamicum (Brevibacterium flavum)
Plasmid pBl1.
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                                                                                                                                                                                                                                                                                                                                                                        Score 326; DB 2;
Pred. No. 1e-17;
                                                       401 AA
                                                                         Created)
                                                      PRT;
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29.1%;
                                                                       (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 29.1
nes 98; Conservative
                                                      PRELIMINARY;
                                                                                                                                                                                                                                lasmid 35:62-66(1996)
                                                                                                                                                                                                                                                           STRAIN=ATCC 21086;
Favey S., Leblon G.,
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=ATCC 21086;
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         401
                                                                                                                                                                                                                       synthetic DNA."
<u>..</u>¥
                                                                                                           Name=repBl1;
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                                                                       01-MAY-2000
                                                                                         01-JUN-2003
Replicase.
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         400
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STANDARD;

REP_STRLI ID REP_STRLI AC P22406;

RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 PISGV-----NGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----REMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV----SENILESF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SDAMFDRWISKLVSLGFAAPLR-----NSGGLDVRKIGGEAD-QVLAAVLTKIA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG--VGMEVGSGDGKSGRHGNRAPWEI --- AVDAVGG--- DPQA----- LELWREFE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 DGKAPALELARADIKTATGGNVAPFELLGRIGDLTGGMTEDDAAGVGSLEWNLSRWHEYE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 170:4634-4651(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76; Gaps
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89008081; PubMed=3170481;
Kendall K.J., Cohen S.N.;
Complete nucleotide sequence of the Streptomyces lividans plasmid plJJ101 and correlation of the sequence with genetic properties.";
J. Bacteriol. 170:4634-4651(1988).
                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 316; DB 1; Length 45 30.5%; Pred. No. 7.5e-17; ive 40; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 GTGSVA-MVTMTMRHTAGQRLHDLWTGLSAAWKAATNGRR-----
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InterPro; IRR000989; Rep.
InterPro; IRV000989; Rep.
Plam; PF01446; Rep.1; I.
Plasmid; Plasmid partition.
SEQUENCE 456 AA; 49617 MW; 0976FD9D9429C7DC CRC64;
(Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 44, Last annotation update)
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Matches 100; Conservative
                                                                                                                                          Streptomyces lividans. Plasmid plui011.
                                                                                                                                                                                                                                                             NCBI_TaxID=1916;
                                                                                        Rep protein.
                             01-AUG-1991
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pIJ101.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

October 22, 2004, 22:14:09 ; Search time 5028 Seconds (without alignments) 10722.008 Million cell updates/sec

Title: Perfect score:

US-10-007-527A-1 1140 1 atgaccagcgtaagtgctga......taatatcggttcgcaagtga 1140 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 4526729 seqs, 23644849745 residues Searched:

9053458

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: 9b ba:*
2: 9b htg:*
4: 9b om:*
5: 9b ov:*
6: 9b ov:*
7: 9b pb::*
9: 9b pb::*
10: 9b pr:*
11: 9b sts:*
11: 9b sts:*
13: 9b un:* GenEmbl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AX548642 Semience	AY178757 Rhodococc	AX548646 Semience	AX548648 Semience	AX548647 Semience	AY180162 Shuttle v	AY150274 Propionib	II83788 Actinomyces	AY172684 Corvnebac	E17316 Bifidobacte	AF085719 Bifidobac			_					
SOMMAKIES		ΠD	AX548642	AY178757	AX548646	AX548648	AX548647	AY180162	AY150274	APU83788	AY172684	E17316	AF085719	AF429315	PFR6662	AF429315	AX655393	SNA243257	AE011844	AF533985	AX826928
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		Match Length DB	1140	6334	6334	9652	11241	11241	3540	2439	4603	2297	5750	125020	2051	125020	2000	9367	13651	12855	1189
*	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	8.3	7.8	4.9	4.5	4.5	4.3	4.1	4.1	3.9	3.7	3.6	3.6	3.6
		Score	1140	1140	1140	1140	1140	1140	94.4	88.8	55.8	51.6	51.6	49	47.2	46.4	44.4	42.4	41.4	41.2	40.6
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AX826927 Sequence AX700509 Sequence	X83601 M.musculus AC121312 Mus muscu		AC111496 Rattus no	Gallus	Gallus	Gallus	Rattus	Rattus						AF092035 Integrati	AF092037 Corynebac	AR173114 Sequence	AR173115 Sequence		Method	Arginin		
A A	0 MMPTX3 AC121312	AC144481	AC111496 AC095394	AC150093	AC150046	AC150059	AC132020	AC127107	AC129703	AY172685	AC092898	AX700512) MMU33842	2 AF092035	AF092037	AR173114	AR173115	BD106940	BD106941	BD139585	BD139586	BLPLASM1
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40.6	40.6 40.6	39.0	38.8	38.6	38.6	38.6	38.4	38.4	38.4	38.2	37.6	37.4	37.4	37,4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4
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ALIGNMENTS

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181 GGTCCGAAAGGTTCTGGATCCGAAGGCCTTCGTTCCTGCGAAAGGGCTGGATCTGCCCC

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Corynebacterineae; Nocardiaceae; Rhodococcus. 1 (bases 1 to 6334) Kostichka,K., Tao,L., Bramucci,M., Tomb,J.-F., Nagarajan,V. and

AUTHORS

Cheng, O. A small cryptic plasmid from Rhodococcus erythropolis: characterization and utility for gene expression Appl. Microbiol. Biotechnol. 62 (1), 61-68 (2003) 22718480

and

12835922 2 (bases 1 to 6334) Kostrochka, K., Tao, L., Brammucci, M., Tomb, J.-F., Nagarajan, V. Cheng, Q.

Direct Submission
Submitted (11-NOV-2002) CR&D, B.I. Dupont de Nemours Inc.,
Experimental Station, Wilmington, DE 19880-0328, USA
Location/Qualifiers

erythropolis"

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AUTHORS

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/db_xxef="texon:1833"
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/note="cryptic plasmid"
complement (1912. 3051)

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/gene="rep" /gene="rep" /note="Rep"

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                                            TGCTGTGCGGGAAAGTCGGTGCACATCGTGCAGACGAAATTTCTCAAGTTGTTGCTCAT
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                                                                                                            TCCGATAAGCGCGCATCCGCCACCACCTCCCAACTTCAACAATCACCACGTCA
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BCT 23-JUL-2003

6334 bp DNA linear BCT 23-JUL-200 erythropolis cryptic plasmid pAN12, complete sequence.

Rhodococcus erythropolis Rhodococcus erythropolis Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS DEFINITION

GI:28628256

AY178757 Rhodococcus e AY178757 AY178757.1

RESULT 2 AY178757/c

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us-10-007-527a-1.rge

ORGANISM Rhodococcus er	Bacteria; Acti Corynebacterin REFERENCE 1 AUTHORS Bramucci,M.G., TITLE Rhodeoccus cl JORNAL Patent: WO 020	E.I. DU PONT D FEATURES Locat Source 16	/mol_ /mol_ /stra /db_x	Query Match Best Local Similarity Matches 1140; Conservat	Oy 1 ATGACCAGCGTA	Oy 61 TCCGATAAGGGC	Oy 121 GAAACATTTAAC 	Oy 181 GGTCCGAAAGGT 	Qy 241 TGCTGTGCGGA 	OY 301 CAACTGGGGACT 	Qy 361 CGGCTCCACGAC Db 2691 CGGCTCCACGAC	Qy 421 CGTTGGCGTACG 	Oy 481 ACTCACGGAAAA Db 2571 ACTCACGGAAAA	Oy 541 GTGAGTGAGAAC Db 2511 GTGAGTGAGAAC	Oy 601 CTGGTATCTCTGG 	
181 GGTCCGAAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAAGGGCTGGATCTGCCCC 240	2871 GGTCCGAAAGGTTCTGGATTCGGAGGCCTTCCTGCGGGAAAGGCTGGTTCTCCCCCC 2812 241 TGCTGTGCGGGAAAGTCGCTGCACATCGTGCACACGAAATTTCTCAAGTTGTTGCTCAT 300 2811 TGCTGTGCGGGAAAAGTCGGTGCACATCGTGCAACATTCTCAAGTTGTTGCTCAT 2752	301 CAACTCGGGACTGGATCTGTTGCGATGGTGACCATGACCATGCGCCATACAGCTGGGG 360 	361 CGGCTCCACGACCTATGGACTGGACAGCCTGGAAAGCTGCGACCAACGGTCGT 420 	421 CGTTGGCGTACGGAACGTGAAATGTACGGCTGCGACGGATACGTGCGCGCTGTTGAAATC 480 	481 ACTCACGGAAAAAACGGCTGGCACGTCCACGCGCTACTCATGTTCAGGTGGTGAC 540 	541 GTGAGTGAGAACATCCTCGAATCCTTCTCGGATGTTCGATGGTGGACTTCCAAA 600 	601 CTCGTATCTCTGGGATTTGCTGCGCCACTACGTAATTCGGGTGGTCTCGATGTACGAAAG 660 	661 ATCGGCGGTGAAGCTGATCAAGTTCTCGCTGGGTATCTGACGAAATTGCATCTGGCGTT 720 	721 GGTATGGAGGTIGGTAGTGGCGACGGAAAAAGTGGTCGACATGGCAACCGTGCACCCTGG 780 	781 GAAATCGCTGTTGATGCAGTGGGCGGAATCCACAAGCGTTGGAACTGTGGCGAGAATTT 840 	841 GAGTITGGITCGAIGGGACGICGGGCAATCGCGTGGTCCCGTGGATTGCGTGCCCGAGCT 900 	901 GGTCTTGGGGCAGAACTAACAGATGCTCAGATCGTTGAGCAGGAAGAATCTGCCCGGTC 960 	961 AIGGITGCGAICATHCCGGCGCGAICGIGGAIGAIGAITGACATHGGGCCTIACGIC 1020 	1021 TICGGCGAGAICCTCGGACTCGTCGAAGCTGGCGACTTGGGAAAATCTTCGTGATCAC 1080 	1081 TTGCATTATCGATTGCCCGCAGCGGATGTGCCGCCCCGATAATATCGGTTCGCAAGTGA 1140 	
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2992 2872 2812 2692 ó 2752 2632 AAACGGCTGGCACGTCCACGTTCACGCGCTACTCATGTTCAGTGGCTGAC 540 180 300 360 420 2392 2331 GGTATGGAGGTTGGTAGTGGCGACGGAAAAGTGGTCGACGTGGCAACCGTGCACCCTGG 2272 240 009 999 780 9 TGGATCTGTTGCGATGGTGACGATGACCATGCGCCATACAGCTGGTCAG AAGTGCTGAACACCTTTCCGGGAAAGACCGGCCTCCCGTCCTCGTGTCG CGCCTGTGGCCGGCCGATTTCTGGCGTGAACGGTGTGACCATTGTCAAC **AAAAGTCGGTGCACATCGTGCAGACGAAATTTCTCAAGTTGTTGCTCAT** CCTATGGACTGGACTTTCGGCAGCCTGGAAAGCTGCGACCAACGGTCGT CCTATGGACTGGACTTTCGGCAGCTGGAAAGCTGCGACCAACGGTCGT ATCCTCGAATCCTTCTCGGATGCGATGTTCGATCGGTGGACTTCCAAA 721 GGTATGGAGGTTGGTAGTGGCGACGGAAAAAGTGGTCGACATGGCAACCGTGCACCCTGG SGGATTTGCTGCGCCACTACGTAATTCGGGTGGTCTCGATGTACGAAAG Gaps inobacteria; Actinobacteridae; Actinomycetales; neae; Nocardiaceae; Rhodococcus. ; 0 100.0%; Score 1140; DB 6; Length 6334; 100.0%; Pred. No. 1e-285; tive 0; Mismatches 0; Indels 0; ., Cheng,Q., Kostichka,K.N. and Tomb,J.F. loning and expression vectors 2055709-A 5 18-JUL-2002; B NEWOURS AND COMPANY (US) tion/Qualifiers 6334 janism="Rhodococcus erythropolis" Ltype="unassigned DNA" cain="AN12" _xref="taxon:1833" rythropolis 원 경 В à ò

781 GAAATCGCTGTTGATGCAGTGGGCGGGGATCCACAAGCGTTGGAACTGTGGCGAGAATTT 840

PAT 27-NOV-2002

linear

DNA

AX548646 6 from Patent W002055709. AX548646 AX548646.1 GI:25813614

RESULT 3
AX548646/C
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VERSION
KEYWORDS
SOURCE

. Rhodococcus erythropolis

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              CGGCTCCACGACCTATGGACTGGACTTTCGGCAGCCTGGAAAGCTGCGACCAACGGTCGT
                               4692 CGGCTCCACGACCTATGGACTGGACTTTCGGCAGCCTGGAAAGCTGCGAACCAACGGTCGT
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/mol_type="unassigned DNA"
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Shuttle vector pRHBR17
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                                                               2211 GAGTITGGTICGAIGGGACGICGGGCAAICGCGIGGGTCCCGIGGAIIGCGIGCCCCAAGCT
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Coganism="Shuttle vector pRHBR17"
/mol type="unassigned DNA"
/db_xref="taxon:214938"
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Sequence 7 from Patent W002055709.
AX548648 AX548648.1 GI:25813616
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Shuttle vector pRHBR17
artificial sequences; vectors.
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I linearize pAN12 cloned into the PvuII site of pBR328"
join(9925. .11241,1. .3590)
/organism="Cloning vector pBR328"
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                                                             5621 Tregecararecregarecregarecregececeaerreggaaaarerregraareae
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Kostichka, K., Tao, L., Brammucci, M., Tomb, J.-F., Nagarajan, V.
                                                                                                                                                                                                                                                                                        Shuttle vector priming artificial sequences; vectors.

1 (bases 1 to 11241)

Kostichka, K., Tao, L., Bramucci, M., Tomb, J.-F., Nagarajan, V.
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Submitted (14-NOV-2002) CR@D, E. I. Dupont de Numours Inc.
Experimental Station, Wilmington, DE 19880-0328, USA
Location/Qualifiers
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A small cryptic plasmid from Rhodococcus erythropolis: oharacterization and utility for gene expression
Appl. Microbiol. Biotechnol. 62 (1), 61-68 (2003)
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/mol_type="genomic DNA"
/db_xref="taxon:221946"
3591. 9924
/organism="Rhodococcus erythropolis"
/mol_type="genomic DNA"
/db_xref="taxon:1833"
/plasmid="pAN12"
/note="cryptic plasmid"
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/mol_type="genomic DNA"
/db_xref="taxon:214938"
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larity 100.0%; Pred. No. 1e-285;
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                                                                             Gaps
                                             Length 11241;
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                                                                           Indels
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                                            Score 1140; DB 6
Pred. No. 1e-285;
Mismatches 0
db_xref="taxon:214938"
                             100.0%; Scu-
100.0%; Pre
                                                                        Conservative
                                                           Similarity
                                                                        Matches 1140;
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DATACDELLPAPSTSSWIVPVGVKPDGSEVVLDLSHPSHILVVGGKTRSGKSSFVYGLL
DQMRHLPYVYAGVDPTGILFNBLGFGMGGDALRSKRITINDDAAAVVOVLSHITDEMD
RKYLLINCEHRDKWSRNDFFESDPGRRII IVILEEPPGLIERLGNFDSARGARSSDRFA
SKAAGLIVGRIAYGEAVGVVLLLYTQRPDAXIIGTBLAQLTTRVTFAQDSDGLRMSH
PELSSEQVKQNSWASGVGFIEADGVIPLTRFRSYRAELTDLHRPGASVGQIDLIQ"
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TSVDTKITRHRKQGRRRTPYPEBVQRPEDFTAERWSGLRKRKGVDFTAGSGGLDWQTA
DSGDEBALLGSTVAKMNSSYDOLGANBETLGGFKKARRGNRTPFQILEDFLDTGSETDLR
DWRTYVSAHGRRLRTWSKGLRDWAGMESBRSDEQVAAQDQCGEAVALFDHDAWRQIR
TAGAAFLLDELELHGSEGVYAWLKKRRIHYEIPLVPWSTST"
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/db xref="G1:27465055"
/translation="MGGQYGILNRGFYNGSHNEIIGGYPMNGRVIVWPDPALLSAMPL
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RSDRHVLHLVLRVPAGLADSAAYLEKGAAEIQRQLRGKKSWRTCIVKPAEHGLDIIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="minivtlskaophdricsehepcaarrseroraadrightrat
fpvsdspcrkpnegrrhryemrdgirnpovmplervrkcgavpvsorialmaghggag
yaglatcgsvwacpvcaakisahrrdblarvvovavglgfkvsmltltorhhagdla
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Bacteria; Actinobacteria; Actinobacteridae; Propionibacterium.
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
Spass 1 to 3540)
Farrar, M.D. and Holland, K.T.
Farrar, M.D. and characterisation of a cryptic plasmid from the skin commensal Propionibacterium granulosum
                                                                                                                                         2 (bases 1 to 3540)
Farrar,M.D. and Holland,K.T.
Direct Submission
Submitted:
Microbiology, University of Leeds, Leeds LS2 9JT, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                               /organism="Propionibacterium granulosum"
/mol_type="genomic DNA"
/strain="PF283"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                             /db xref="taxon:33011"
/plasmid="cryptic plasmid pPG01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="plasmid transfer protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAN78123.1"
/db_xref="GI:27465057"
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/codon start=1
/trans1_table=11
/product="Orf3"
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trans1 table=11
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/gene="rep"
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/gene="rep"
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/gene="tra"
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               GGTCCGAAAGGTTCTGGATTCGCAGGCCTTCGTTCCTGCGGAAAGGGCTGGATCTGCCCC 6402
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                                                                                                                           CAACTCGGGACTGGATCTGTTGCGATGGTGACGATGACCATGCGCCCATACAGCTGGTCAG
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                                                                                         6401 TGCTGTGCGGGAAAAGTCGGTGCACATCGTGCAGACGAAATTTCTCAAGTTGTTGCTCAT
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/trānslation="MFFIGKYRTKFQPIAPCKPSPIFDGNGKRTGEFSSEKMRTQAIT
EDGRLVELTSIPPQFVQLIDDAVKSRELLEFEKVNLAVLPRNGGGISTYLTLGEAVHV
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TPTEALESCEKLYWFFEPRLVDVVLHEVGECRCAGTNSAVARSLSSRAFIPARFVQS
LENGGRNPAQLITQDQVAGMRKTLGTR"
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Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacterium.
1 (Bases I to 4603)
1 (Bases I to 4603)
1 (Bases In Obrynebacterium glutamicum and Thierbach, G.
Plasmids in Corynebacterium glutamicum and their molecular
classification by comparative genomics
22830013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY172684 4603 bp DNA circular BCT 05-
Corynebacterium glutamicum plasmid pAG3, complete sequence.
AY172684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2378. .2406
/note="double stranded origin; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88.8; DB 1;
Pred. No. 6.1e-12;
0; Mismatches 152;
                                                                                                                                                   /protein_id="AAC46400.1"
/db_xref="GI:1805290"
                                                                                                                                  /product="unknown"
                                                                                                                                                                                                                                                                                                                                                  'product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Scor.
55.5%; Pred
0; }
                                                                                                                  table=11
                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                1673. .1676
1685. .2023
/note="ORF112"
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                                                                                                                                                                                                                                                                                       /note="ORF129"
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                                                                                                                                                                                                                                PAPVVVEVSE"
                DWSLPPKIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA circular BCT 15-JUN-1998 complete plasmid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases I to 44.9)
Billington, S.J., Jost, B.H. and Songer, J.G.
The Arcanobacterium (Actinomyces) pyogenes plasmid pAP1 is a member of the piJ101/pJV1 family of rolling circle replication plasmids
J. Bacteriol. 180 (12), 3233-3236 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSDERSRDKEROI PSYRREGRSATHPICATVITTEPVSNESKKTAKSRRSERYELRDG
LAEISTIESVRKCGRVPVAPLVSLRAKSDGKCAGGGGLHTCGSVWACPVCSAKIAARR
TYDLQQVVPRANTHYRGMTVSMLTLTQRHHKGGGLKHUMDALSTAWNRVTSGRRWIEFKE
OFGLVGYVRANEI THGKHGWHVHSHVLI ISEKDPLITSTFVYORKGGRERLPYPPBIYM
SSDFIAERWEAGLLAKHGVDFLRDSGGLDWTVKDARAIGIGNYVSKMGTSTDAISSEVTL
GGFKKARNGNFIPFOILADILSLGDVDDLKLWKEYEKASFGRRALTWGKGLRDWANLG
VEQSDEEIASBEIGDEAIAFTHDAWRQVRRFGAAELLDVTESGGRAAAYRWLDFREI
                                                                                       357
241 TGCTGTGCGGGAAAAGTCGGTGCACATCGTGCAGACGAAATTTCTCAAGTTGTTGCTCAT 300
                                                                                                                                                                 417
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                                                                                                            2387 GCGGTTGGACTCGGCTTCAAGGTGTCGATGCTGACGCTTACTCAACGTCATGCTGGT
                                                                                                                                                                                             2447 caggarcricgccgagcrigrigggcgcgcrccagrcggardgaargcrigrcacaggg
                                                                                                                                                                                                                                                                       2507 cGacGGTGGCAGGAATTTTGCGCTCAGCTCGGCGTCCAGGATGGGTCAAGGCAGTTGAA
                                    2327 Gréréredecaaagarrrecedecaccercardareageregecegerirereageri
                                                                           301 CAACTCGGGACTGGAT---CTGTTGCGATGGTGACGATGACCATGCGCCATACAGCTGGT
                                                                                                                                                       CAGCGGCTCCACGACCTATGGACTGGACTTCGGCAGCTGGAAAAGCTGCGACGGT
                                                                                                                                                                                                                                  CGTCGTTGGCGTACGGAACGTGAAATGTACGGCTGCGACGGATACGTGCGCGCCTGTTGAA
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Bacteria, Actinobacteridae, Actinomycetales,
Actinomycineae, Actinomycetaceae, Arcanobacterium,
L. (bases 1 to 2439)
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                                                                                                                                                                                                                                                                                                                          529
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                                                                                                                                                                                                                                                                                                                478 ATCACTCACGGAAAAAACGGCTGGCACGTCCACGTTCACGCGCTACTCATGT

    .110
    /note="single stranded origin; putative"

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Direct Submission
Submitted (06-JAN-1997) Veterinary Science, Uni
1117 East Lowell Street, Tucson, AZ 85721, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arcanobacterium pyogenes"
/mol_type="genomic DNA"
/strain="BBR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APU83788 2439 bp
Actinomyces pyogenes plasmid pAP1,
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/plasmid="pAP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arcanobacterium pyogenes
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221. .1600
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TITLE
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JOURNAL
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E17316

E17316

E17316

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E17316.

E17316.
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MAIQHARINSVFGYNLRIMYKALDDRKAIFNHWVNVTRSDADYDMEVPVTVFVPPFKP
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translation="MATTPSKPFRGLAEQLEKVRSSLEVIASNVNADHDLSDDGKNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 GICCACGITCACGCGCTACTCATGTTCAGTGGTGACGTGAGTGAGAACATCCTCGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 TTCTCGGATGCGATGTTCGATCGGTGGACTTCCAAACTCGTATCTCTGGGATTTGCTGCG
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C12N15/09, (C12N15/09, C12R1:19), (C12N15/09, C12R1:01); CC
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4.9%; Score 55.8; DB 1; Length 4603;
Best Local Similarity 54.0%; Pred. No. 0.0024;
Matches 114; Conservative 0; Mismatches 97; Indels 0
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topology: Linear;
Location/Qualifiers
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387. .392
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CC topology: Linear;
FH Key
FT source
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BYGSPVASSYLGSRRAMENDALQAWANGAGGLFSFSPSBKQRGVSVNPVV
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VGRGAWGALASPTFRRAVILDDAVAATDSAEGBARAARDVLKLFGVAHTVTAIGLAKTT
LDTVLFTHTDVFKRELHEAVWSGRKQTALPVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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KAELEQQLKDMQQALKEQQQLAFNAREELEQQRNLKPVVVTVRVPQYVRDEMKRLAAI
                                                                 Tauch, A., Puchler, A., Kalinowski, J. and Thierbach, G. Direct Submission Submitted (05-NOV-2002) Department of Genetics, University of Bielefeld, Universitatesstrasse 25, Bielefeld D-33615, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="repA"
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                                                                                                                                                                                                                                                                                           1. .4603
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/strain="22220"
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/db_xref="G1:4972587"
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ILFDTVIRQSTRYSKPFGHTPKKTYDYADAWQEIQKAGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QWLLDRWKTMVKRVAKAYKKKDGNPYNVAPNDEHGIDLQFKSGKDAGTAAAEYITKIQ
GDKGGVTLAQEIARGDIKNGRMGSVNPPQLLDSGCLGLSDFQREDLWLEYWQATLRRR
CITWSRGLKEDMEVEELEDEELAEKADELPGLVGYVVPNRVYKDIRKSAPETLADALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTSGVVVGGIPGSGKTAGMNVIVLALYLSGCCNIHVIDGKGGDDWGWFSEHATTFVTG
DLDTVHDTLIKLDDEMKCRIASMRQRYGSANYWNVQPDKRPPLEVIIIDECQSFFNAK
GILGGKPAKDKAEBITAAATEIVQKGRSGGFLLFALTQKPTTDSLPSALRENCENRIC
FRVKTPEAARAVLGDMPDGSPSPTDIPPARRGGAIIGLATGEDVMCRFAYVSEEEAER
AVVANHKGVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MTNGEKARFTGTMLCGSIWACPTCSAIIRHERAHEVALAIGNHA
EKLRKAAADQWQAEHEGQRLPPELMVSDSFGNYIFGTLTLRHDRTMPLAMTLDAILKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKWPWNHNTKPEPLPFRLRPFDPATGGITVGKLANGNDATLIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; similar to transfer proteins
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                                                                                                                                                                                                                                                     /Jobe="Rep; similar to replication proteins of Streptomyces plasmids and other members of the pC194 family that replicate by a rolling circle mechanism"/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAEREDWOEVARLLPGGVILTDEQODAIADGEAKPGDYLPTKGVWV.
complement (3926. 3334)
/note="region conforming to double stranded origin;
nicking site of rolling circle plasmids"
complement (3985. 4845)
/gene="frak gene homolog"
/gene="frak gene homolog"
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                      /product="replication protein"
/protein_id="AAD34709.1"
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                                                                                                                                                                                          /note="replication gene"
complement(2373. .3515)
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/transl_table=11
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1 (bases 1 to 5750)
0'Riordan,K. and Fitzgerald,G.F.
Molecular characterisation of a 5.75-kb cryptic plasmid from Bifidobacterium breve NCFB 2258 and determination of mode of
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O'Riordan,K. and Fitzgerald,G.F.
Direct Submission
Submitted (22-AUG-1998) Microbiology, Univeristy College Cork,
Western Road, Cork, Ireland
Location/Qualifiers
signal 410. .415
525. .530
539. .2023
/product='replication protein of pNBbl'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              putative involvement in plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF085719 5750 bp DNA circular BCT Bifidobacterium breve plasmid pCIBb1, complete sequence.
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                                                                                                                                                                                                                                                        Length 2297;
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                                                                                                                                     /organism="Bifidobacterium breve"
/mol type="genomic DNA"
/db xref="taxon:1685"
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/transl_table=11
/product="partitioning protein"
                                                                                                                                                                                                                                                   Score 51.6; DB
Pred. No. 0.03;
); Mismatches
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/note="partitioning gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 GCGATGTTCGATCGGTGGACTTCCAAACTC
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/strain="NCFB 2258"
/db_xref="taxon:1685"
/plasmid="pCIBb1"
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52.9%;
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Bifidobacterium breve
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Propionibacterium freudenreichii plasmid pLME108 rep gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dasen,G.H., Miescher,S., Teuber,M. and Meile,L.
Molecular analysis of plasmid pLME108, a plasmid isolated from
Propionibacterium freudenreichii
Unpublished
                                                                                                                                                   GCTCAGATCGTTGAGCAGGAAGAATCTGCCCCGGTCATGGTTGCGATCATTCCGGCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-UTM-1998) Dasen G.H., Institute of Food Science, Laboratory of Food Microbiology, ETH Zurich, LFO G24.2, Schmelzbergstr. 9, CH-8092 Zurich, SWITZERLAND Location/Qualifiers
                                                                                                           507 CCACGTTCACGCGCTACTCATGTTCAGTGGTGACGTGAGAACATCCTCGAATCCTT
                                                                                                                                                                                                                                                                                                                                                                                        567 CTCGGATGCGATGTTCGATCGGTGGACTTCCAAACTCGTATCTCTGGGATTTGCTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 ACTACGTAATTCGGGTGGTCTCGATGTACGAAGATCGGCGGTGAAGCTGATCAAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTGCGTATCTGACGAAAATTGCATCTGGCGTTGGTATGGAGGTTGGTAGTGGCGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATCCACAAGCGTTGGAACTGTGGCG--AGAATTTGAGTTTGGTTCGATGGGACGTCGG
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Propionibacterium freudenreichii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium

    2051 / Organism="Propionibacterium freudenreichii"

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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
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Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L. Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
                                                                                                                                                                                        Craniata, Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)

14 (bases 2 to 125020)

15 (bases 1 to 125020)

16 (bases 1 to 125020)

17 (bases 1 to 125020)

18 (bases 1 to 125020)

19 (bases 1 to 125020)

10 (bases 1 to 125020)

10 (bases 1 to 125020)

10 (bases 1 to 125020)

11 (bases 1 to 125020)

12 (bases 1 to 125020)

13 (bases 1 to 125020)

14 (bases 1 to 125020)

15 (bases 1 to 125020)

16 (bases 1 to 125020)

17 (bases 1 to 125020)

18 (bases 1 to 125020)

19 (bases 1 to 125020)

19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .125020
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Mol_xref="taxon:9606"
// Chromosome="16"
// map="16024.3; between D16S520 and WI-12410"
// note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 12.33; rrev. wv. v..., Matches 114; Conservative 385; Mismatches 419; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (35581. .35746)
/rpt_type=tandem
/rpt_unit="ctg"
complement (<36507. .>36887)
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/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (<36507. .36887)
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/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="junctophilin 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="synonym: JP3"
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                                                   GI:17646244
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                                                                                                                  Homo sapiens (human)
                                                                                                                                                          Homo sapiens
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              AF429315
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GSVWACPVCNAKIMARRGLELGAAVETWTKHGGRVAFWTFTVRHSRKDSLTAVMDGVA
SGWRRVTSGRGWTSDQLRHGVBGFVRVVEVTHGRNGWHVHLHVLVFLVGDFGDALALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSMFGRWERGVLAAGLGTPLARAQDVQQMSAATGLDHLARYLSKAQFQGKIGHELTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSKTARSALSTRSTWEVLGDAANGLAKEVGLWFEWEKGSRGRRQIGWSAGLRDRLGLM
VEESDDVIAABEVGSVADTVALITGDGWRRLVGQQKLYECLRSCELGGQAGLARWLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1094 AGATCATGGCTCGGCGTGGCCTTGAACTCGGCGCGGCGGTCGAGACTGGACTAAGCACG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVVDARARSRGVRGCGGGSPAVAPLGGALDNHANNVSPSAVPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 -TGGATCTGTTGCGATGGTGACGATGACCATGCGCCATACAGCTGGTCAGCGGCTCCACG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1034 Gregororiorica de de contra de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 ACCTATGGACTGGACTTTCGGCAGCCTGGAAAGCTGCGACCAACGGTCGTCGTTGGCGTA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974 CTGTTTGGGATGGTGTCGCTTCGGGGGGGGGGGGGGCTCACTTCGGGCCAAGGGCTTGGACGT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cráaccaccrccarcacagarcaagacrircaracararcarcaagarracacacacaec 855
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[ (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Florersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTCGGTGCACATCGTGCAGACGAAATTTCTCAAGTTGTTG-CTCATCAACTCGGGAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47.2; DB 1; Length 2
Pred. No. 0.42;
0; Mismatches 178; Indels
                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
/product="putative rep protein"
/protein_id="CAA07175.1"
/db_xref="GI:3212128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125020 bp
Homo sapiens junctophilin 3 (JPH3)
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GOA:069764"
/db_xref="TrEMBL:069764"
                                                                                           /plasmid="pLME108"
complement(223. .1434)
                                                                                                                                                                                         complement (223. .1434)
_type="genomic DN
xref="taxon:1744"
                                                      lab host="DF2
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Best Local Similarity 49.4%;
Matches 177; Conservative
                                                                                                                                                                  dene="reb"
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Matches
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VERSION
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50702 TGVMRWVGYGBCDTHVTYDGGHHGSWGMMKSCGYSDBGKCAKBGSKMCTGSMTKYTCYGY 50761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGYCTGFKGQGEYTCSWS
HGFEVLGYYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 AGTIGITGCTCATCAACTCGGGACTGGATCTGTTGCGATGGTGACGATGACCATGCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50762 GKYWSSKSADBSYYYSBSHYBWGSYMCCRKBSYASSYDVRYYKBTGMYRYVRSCSWYYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GACCATTGTCAACGGTCCGAAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGATCTGCCCCTGCTGTGCGGGAAAGTCGGTGCACATCGTGCAGACGAAATTTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 CGACCAACGGTCGTTGGCGTACGGAACGTGAAATGTACGGCTGCGACGGATACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50882 DVDRCYACSSBMKYKMHRKKHYKKDSHBSWGKSHMKKGAWRVRSMYRSMRCSVHDSSMVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGCTGTTGAAATCACTCACGGAAAAAACGGCTGGCACGTCCACGTTCACGCGCTACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                              /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                                                                          Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="junctophilin 3"
complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                                                                                                   complement (35581. .35746)
                                                                                                                                               1. .125020
/organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym: JP3"
                                                                                                                                                                                                                                                                                                                                                           rpt_type=tandem
                                                                                                                                                                                                                                             /chromosome="16"
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                                                                                                                                                                                                                                                                                                                                                                                                                            gene="JPH3"
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Matches 95; Conserv
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TGTACGAAAGATCGGCGGTGAAGCTGATCAAGTTCTCGCTGCGTATCTGACGAAAATTGC 710
                                         274 SYGWYSWSYKWWMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRWAMMYKKMYWYR 333
                                                                                                                                                                771 TGCACCCTGGGAAATCGCTGTTGATGCAGTGGGCGGGGATCCACAAGCGTTGGAACTGTG 830
                                                                                                               334 GYKGMKRGWWAGRMMRSMCRWSKACYYMRWRMTMTRRRRWAKKSSRTSRKKKRKWCMR
                                                                                                                                                                                                                                                                                                                                        454 YKWASHNYRWRKKKCSRITIMWGKIRGGMMGIMGRCRYKKRSGMKRKCRRRRWGRMYRMRW
                                                                                         ATCTGGCGTTGGTATGGAGGTTGGTAGTGGCGACGGAAAAAGTGGTCGACATGGCAAACG
                                                                                                                                                                                       831 GCGAGAATTTGAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTCCCGTGGATTGCG
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574 KYSKCS 579
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Patent: WO 03000989-A 5563 03-JAN-2003;
Syngenta Participations AG (CH)
                                                                          904
                                                                                                                                                                                                                                                                                                   988
                                                                                                                                                                                                                                                                                                                                                                             TGCGTGCCCGAGCTGGT-CTTGGGGCAGAACTAACAGATGCTCAGATCGTTGAGCAGGAA 945
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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GGTGGACTTCCAAACTCGTATCTCTGGGATTTGCTGCGCCACTACGTAATTCGGGGTGGTC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                534 TGGTGACGTGAGTG---AGAACATCCTCGAATCCTTCTCGGATGCGATGTTCGATCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GSCKRKKSKGGSWGKTCRRGARGGSGWSSGAKYKSGSMSKRMWMSSCGRSGCGRRSAYSR
                                                                                                                                                                                                                                                                                                   TGTGGCGAGAATTTGAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTCCCGTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 TGAAATCACTCACGGAAAAAAGGGCTGGCACGTCCACGTTCACGCGCTACTCCATGTTCAG
                                                                          TCGATGTACGAAAGATCGGCGGTGAAGCTGATCAAGTTCTCGCTGCGTATCTGACGAAAA
                                                                                                                                                  707 TTGCATCTGGCGTTGGTATGGAGGTTGGTAGTGGCGACGGAAAAAGTGGTCGACATGGCA
                                                                                                                                                                                                                          767 ACCGTGCACCCTGGGAAATCGCTGTTGATGCAGTGGGCGGGGATCCACAAGCGTTGGAAC
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3.9%; Score 44.4; DB 6; Length 20
Best Local Similarity 10.1%; Pred. No. 2.3;
Matches 55; Conservative 246; Mismatches 242; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   946 GAATCTGCCCCGGTCATGGTTGCGATCATTCCGGCG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5263 from Patent WO03000898. AX655393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
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ACCESSION
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SOURCE
ORGANISM
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5.1.6 Compugen Ltd.	
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	using sw model
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October 22, 2004, 22:12:19 Run on: ₹

; Search time 637 Seconds (without alignments) 9394.568 Million cell updates/sec

l atgaccagcgtaagtgctga......taatatcggttcgcaagtga 1140 US-10-007-527A-1 1140 score: Sequence: Title: Perfect

4134886 seqs, 2624710521 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

8269772 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s:*
genesequ200s:*
genesequ2001s:*
genesequ2001s:*
genesequ2001bs:*
genesequ2002as:* geneseqn2003cs:* geneseqn2003ds:* N_Geneseq_23Sep04:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

		Description	Abg76122 Rhodococc	Abd76124 Rhodococc	Abd76126 Plasmid n	Abd76125 Plasmid n	Adh10182 E. coli-P	Aav58945 B. breve	Ada71938 Rice gene	Achoose Mirine Pr	Achooseo Murine PT	Acc00046 Mouse PTX	Acc00048 Mouse ups	Aaa90951 B. lactof				Aad22583 B. lactof		Adb66212 B. lactof	2108	Ada71938 Rice gene	Acal8944 Prokaryot	
SUMMARIES		QI	ABQ76122	ABQ76124	ABQ76126	ABQ76125	ADH10182	AAV58945	ADA71938	ACH00861	ACH00860	ACC00046	ACC00048	AAA90951	AAA90934	ABL49734	ABL49733	AAD22583	AAD22582	ADB66212	ADA71779	ADA71938	ACA18944	
		图	9	9	9	9	12	7	œ	10	10	σ	œ	ო	m	9	9	9	9	10	8	80	œ	
		Length DB	1140	6334	9652	11241	11241	2297	2000	1189	1244	1841	2708	4447	4447	4447	4447	4447	4447	4447	2000	2000	498	
de	Query	Match	100.0	100.0	100.0	100.0	100.0	4.5	3.9	3.6	3.6	3.6	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.2	3.5	3.1	
		Score	1140	1140	1140	1140	1140	51.6	44.4	40.6	40.6	40.6	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	36.6	36.4	34.8	
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34.8	34.8	34.8	34.8	34.6	34.6	34.4	34.2	34.2	34.2	34.2	34.2	34.2	34	34	34	33.8	33.6	33.6	33.6	33.6	33.6	33.6	33.6
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ALIGNMENTS

Rhodococcus AN12 replication protein Rep DNA. ABQ76122 standard; DNA; 1140 BP 13-JAN-2003 (first entry)

Plasmid stability protein; replication protein; ethylene forming enzyme; carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase; polyhydroxyatkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase; gene; shuttle vector; Rep; ds.

Rhodococcus erythropolis

WO200255709-A2.

18-JUL-2002.

12-DEC-2001; 2001WO-US047868.

12-DEC-2000; 2000US-0254868P.

Tomb J; Kostichka KN, Bramucci MG, Cheng Q,

Е І.

(DUPO) DU PONT DE NEMOURS & CO

WPI; 2002-557827/59. P-PSDB; ABB84278.

New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.

Claim 2; Page 63-64; 96pp; English.

This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isoprenoid molecules, polyhydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile

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Sequence 6334
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       dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence encodes the Rhodococcus ANI2 Rep protein described in the disclosure of the invention
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decarboxylase, alcohol
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Plasmid stability protein; replication protein; ethylene forming en; carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase; polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase; shuttle vector; circular; ds.

(first entry)

13-JAN-2003

Plasmid pRHBR17 DNA

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New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.

٦, Tomb

Kostichka KN,

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Bramucci MG,

WPI; 2002-557827/59

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(DUPO) DU PONT DE NEMOURS & CO

12-DEC-2001; 2001WO-US047868 12-DEC-2000; 2000US-0254868P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isoprenoid molecules, polythydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile dehydrogenase, terpene synthases, and choleschool oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents the Plasmid pRHBR17 DNA described in the disclosure of the invention
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ilarity 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                 The invention relates to production of aryl carotenoid compounds. The method involves transforming a host cell comprising a cyclic carotenoid having at least one beta-ionone ring with a gene encoding a carotene desaturase (CrtU) followed by growing the transformed host cell. Also provided is a method for regulating aryl carotenoid biosynthesis in a host cell. The method is useful in the production of aryl carotenoids pharmaceuticals, food supplements, animal feed additives, food colorants and cosmetics. The present sequence represents a E. coli-Rhodococcus shuttle plasmid pRHBR17 nucleotide sequence
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1184 GGCTGGACGAAGATTAACGGAAGCCCTTGGCAACGGGCCTCGGAACGTTGGAAATC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1244 AGGGGTTTCGTCCGCGCGATTGAAATCACCTACGGTGTAAACGGCTGGCACCCTCACATT 1303
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                                                                                                                                                                         used in the vector of the invention. The vector is a shuttle vector for a Bildobacterium, and contains: (a) a replicated essential region originated from a plasmid pNBD1 of Bildobacterium breve ATCC 15698; (b) a replicated essential region originated from a plasmid of B. coli; and replicated essential region originated from a plasmid of B. coli; and on antibiotic-resistant gene originated from a plasmid of B. coli and an antibiotic-resistant gene functioning by a Bifidobacterium. The shuttle vector can be used to transform various Bifidobacteria species
                                                                  contains specific elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 CACGCCTACTCATGTTCAGTGGTGACGTGAGTGAGAACATCCTCGAATCCTTCTCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                            394 GCCTGGAAAGCTGCGACCAACGGTCGTTGGCGTACGGAACGTGAAATGTACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 GACGGATACGTGCGCGCTGTTGAAATCACTCACGGAAAAACGGCTGGCACGTCCACGTT
                                                                                                                                                          sequence represents the essential region gene from plasmid pNBbl
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                     Length 2297;
                                                                                                                                                                                                                                                                                                                    Sequence 2297 BP; 524 A; 659 C; 689 G; 425 T; 0 U; 0 Other;
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Zhu
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Xie Z,
                                                                                                                                                                                                                                                                                                                                                    4.5%; Score 51.6; DB 2;
52.9%; Pred. No. 3.5e-05;
Live 0; Mismatches 99;
                                                                    Shuttle vector for a Bifidobacterium species - c
from existing plasmids e.g. pNBb1 of ATCC 15698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1364 TGGCTGCTCGATCGCTGGAAAACCATGGTC 1393
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Whitham S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGATGTTCGATCGGTGGACTTCCAAACTC
                                                                                                                          Disclosure, Page 14-15; 17pp; Japanese.
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Best Local Similarity 52.9°
Matches 111; Conservative
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                  WPI; 1998-587288/50.
P-PSDB; AAW73071.
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                                                                      Shuttle vector
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Katagiri
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GTGAGTGAGAACATCCTCGGATCCTTCTCGGATGCGATGTTTTGATCGGTGGACTCCAAA
                                                                                                                                                ATCGCCGTGAAGCTGAAGTTCTCGCTGCGTATCTGAAAATTGCATCTGGCGTTT
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                                                     CTCGTATCTCTGGGATTTGCTGCGCCACTACGTAATTCGGGTGGTCTCGATGTACGAAAG
                                                                                                                              ATCGGCGGTGAAGCTGATCAAGTTCTCGCTGCGTATCTGACGAAAATTGCATCTGGCGTT
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410. .415
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Mouse; PTX3; his1; PTX3/his1; long
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                                      Mus sp.
Synthetic.
                 vaccine;
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                                                                 involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unlinfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                 34 SSRMSRKMGSMSKYRKCSSCGKCKMTTRRKSKWYSASSASGRTGSKWSSGSYSGKGMKKR
                                                                                                                                                                                                                                                                                                                                                                              GSCKRKKSKGGGWGKTCRRGARGGSGWSSGAKYKSGSMSKRWWASSCGRSGCGRRSAYSR
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                                                                                                                                                                                                                                           <u>ب</u>
                                                         (M1) for identifying
                                                                                                                                                                                                                 Query Match 3.9%; Score 44.4; DB 8; Length 2000; Best Local Similarity 10.1%; Pred No. 0.0064;
                                                                                                                                                                                          Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                         55; Conservative 246; Mismatches 242; Indels
                                                          present invention relates to a method
                                 27; SEQ ID NO 5263; 899pp; English
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                                                                                                                                                                  illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New derivatives of human or murine pentraxin-3, useful for preparing autologous vaccines for treating tumors, also new nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to derivatives of murine and human pentraxin.3 (PTX3) (shown in ABG75068-ABG75073). These sequences, and biotinylated derivatives of PTX3, are used to make autologous vaccines, based on inactivated tumour cells, to treat solid or haematological tumours. The present sequence is a derivative of the murine PTX3 cDNA shown in the exemplification of the invention
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pentraxin-3; autologous vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; PTX3; his1; PTX3/his1; long pentraxin-3; autologous vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCCGAGGCGACAGTGCCTGGCCTAGGCGCTGTGCTGGAGGAACTGCGGC 486
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Pred. No. 0.081;
0; Mismatches 119;
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                                                                                                                                                        cocation/Qualifiers
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                             cancer; cytostatic; gene;
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Use of recombinant human pentraxin 3 gene and protein for preparing a medicament for increasing the reproductive ability in a female subject, or for diagnosing or treating female infertility.
                                                                                                                                                                                (SIGT ) SIGMA-TAU IND FARM RIUNITE SPA.
                                                               /product= "PTX3 mouse"
                              Location/Qualifiers
144. .1286
/*tag= a
                                                                                                                                                        03-AUG-2001; 2001US-0309472P.
                                                                                                                                   2002WO-IT000473
                                                                                                                                                                                                                          WPI; 2003-239472/23.
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                                                                                                                                   18-JUL-2002;
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                                                                                                                                                                                                                                                                                   New derivatives of human or murine pentraxin-3, useful for preparing autologous vaccines for treating tumors, also new nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                    The present invention relates to derivatives of murine and human pentraxin-3 (PTX3) (shown in ABG75068-ABG75073). These sequences, and biotinylated derivatives of PTX3, are used to make autologous vaccines, based on inactivated tumour cells, to treat solid or haematological tumours. The present sequence is a derivative of the murine PTX3 cDNA shown in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.6; DB : Pred. No. 0.083;
                                                                                       /product≈ "modified PTX3"
                                                                                                                                                                                                      (SIGT ) SIGMA-TAU IND FARM RIUNITE SPA.
  vaccine; cancer; cytostatic; gene; ss.
                                                     Location/Qualifiers
72. .1235
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P-PSDB; ABG75068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2003
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Synthetic
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                                                                                                                                                                      invention relates to the use of recombinant human pentraxin
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Disclosure; Page 54; 63pp; English.
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Best Local Similarity 48.5%;
Matches 112; Conservative
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us-10-007-527a-1.rng

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Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                     fermentation.
                                                                                                                                                16-MAR-1999;
                                                                           EP1038966-A1
                                                                                                   27-SEP-2000.
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15-JAN-2001
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                                                                                                                                                                                                                            Use of recombinant human pentraxin 3 gene and protein for preparing a medicament for increasing the reproductive ability in a female subject, or for diagnosing or treating female infertility.
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 pentraxin 3; PTX3; reproductive ability; antiinfertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 2708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2708 BP; 667 A; 704 C; 640 G; 697 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               mouse PTX3 upstream regulatory region nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.4;
Pred. No. 1.
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                                                                                                                                                       (SIGT ) SIGMA-TAU IND FARM RIUNITE SPA.
                                                                                                                                                                                                                                                                             Disclosure; Page 57-58; 63pp; English.
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                                                                                                        18-JUL-2002; 2002WO-IT000473
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Best Local Similarity
                                                         WO2003011326-A1
 Mouse pentrax infertility;
                                                                                                                                                                               Mantovani A;
                                                                                 13-FEB-2003
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15-JAN-2001
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This sequence encodes the Brevibacterium lactofermentum pSFK6 protein.

The invention relates to a plasmid containing a temperature sensitive replication control region (TSRCR) and a marker gene (MG). The TSRCR is derived from plasmid pAM30 harboured by Brevibacterium lactofermentum (ATCC 13869) and allows the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at an elevated temperature in coryneform bacterium which may be used for medifying a chromosomal gene in a coryneform bacterium, which may be used for the promoterion of useful substances, such as amino acids, by fermentation, to change their genetic traits. Therefore, the plasmid can be used for breeding microorganisms for the production of amino acids by fermentation. The plasmid comprises a TSRCR that allows the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. (Updated on 15 SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmids containing a temperature sensitive replication control regions useful for breeding microorganisms for the production of amino acids by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamatsu T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 19-22; 29pp; English.
Location/Qualifiers
1318. .2601
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                                                                                                                                                                                                                                                                                                                                                                        (AJIN ) AJINOMOTO CO
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nes 80; Conserv
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(first entry) (revised)

29-AUG-2003 29-MAY-2002

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introprecion relates to a plasmid containing a temperature sensitive replication control region (TSRCR) and a marker gene (WG). The TSRCR is derived from plasmid pAM330 harboured by Brevibacterium lactofermentum (ATCC 13869) and allows the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at a low temperature but does not allow materia within a temperature range in which the bacteria can grow. The plasmid can be used for modifying a chromosomal gene in a coryneform bacterium, which may be used for the production of useful substances, such as amino acids, by fermentation, to change their genetic traits. Therefore, the plasmid can be used for breeding microorganisms for the production of amino acids by fermentation. The plasmid comprises a TSRCR that allows the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. (Updated on 15 c SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence encodes the Brevibacterium lactofermentum p48K protein. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 AACGGCTGGCACGTCCACGTTCACGCGCTACTCATGTTCAGTGGTGACGTGAGAAC
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              Temperature sensitive plasmid; TSRCR; protein production; temperature sensitive replication control region; p48K; ds
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1318. .2601
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                                                                                                                                                                                                                                                                                                                                                                                       Kimura
                                                                                                                                                                                                                                                                  16-MAR-2000; 2000EP-00105326.
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Local Similarity 53.0%;
Les 80; Conservative
                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO CO INC.
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The present invention describes a method for transforming a high temperature-resistant coryneform microbe in which the high temperature-resistant coryneform microbe in which the high temperature-resistant coryneform microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall of a microbe having a changed structure of cell wall cresistant coryneform microbe in which the cell wall of a high temperature-resistant coryneform microbe is weakened and electric pulse is applied to a solution containing the microbe having weakened cell wall and a DNA; to a solution containing the microbe having weakened cell wall and a DNA; to a solution containing the microbe having weakened cell wall and a DNA; to a solution containing the microbe carrying both a plasmid vector temperature-resistant coryneform microbe in which a recombinant DNA is introduced, and (3) a transformant of a high temperature-resistant coryneform microbe and coryneforming a high temperature-resistant coryneform coryneform coryneform microbe. The present sequence encodes a Brevibacterium actober microbe. The present sequence microdes a sample from the present invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                             Brevibacterium lactofermentum p48K nucleotide sequence SEQ ID NO:7.
                                                                                      Kanamycin resistant gene; mutation; high temperature resistance; coryneform microbe; transformation; gene; ds.
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                                                                                                                                                                                        Location/Qualifiers
1318. .2601
/*tag= a
                                                                                                                                                                                                                                                  /product= "p48K"
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Best Local Similarity 53.0%;
Matches 80; Conservative
                                                                                                                                                     Corynebacterium glutamicum
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P-PSDB; ABB06342.
                                                                                                               coryneform microbe;
                                                                                                                                                                                                                                                                                           JP2002017362-A
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RESULT 15

613 GGATTTGCTGCGCCACTACGTAATTCGGGTG 643

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ABL49734 standard; DNA; 4447 BP

ABL49734;

RESULT 14
ABL49734
ID ABL497
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AC ABL49

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The present invention describes a method for transforming a high temperature-resistant coryneform microbe in which the high temperature-resistant coryneform microbe and an electric pulse is applied to structure of cell wall of the microbe and an electric pulse is applied to a solution containing the microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall coryneform microbe in which the cell wall of a high temperature resistant coryneform microbe is wakened and electric pulse is applied to a solution containing the microbe having weakened cell wall and a DNA; (2) a transformant of a high temperature-resistant coryneform microbe in which a recombinant DNA is introduced; and (3) a transformant of a high temperature-resistant coryneform microbe in which a recombinant DNA is introduced; and (3) a transformant of a high temperature-resistant coryneform microbe and coryneform microbe and coryneform microbe and a plasmid vector derived from Coryneform microbe and so plasmid vector derived from Coryneform microbe. The present sequence encodes a serious example from the present invention. (Updated on 29-AUG-2003 to a standardise OS field)
                                                                                                                                                            Brevibacterium lactofermentum pSFK6 nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transformation of high temperature-resistant coryneform microbe and
                                                                                                                                                                                                    Kanamycin resistant gene; mutation; high temperature resistance; coryneform microbe; transformation; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                  /product= "pSFK6"
                    ABL49733 standard; DNA; 4447 BP.
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(first entry)
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                                                                                                  29-AUG-2003
29-MAY-2002
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                                                            ABL49733;
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1795 AACGGTTGGCACTTGCACGCAACATGCTGTTGTTCTTGGATCGTCCACTGTCTGACGAT 1854

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493 AACGGCIGGCACGICCACGIICACGCGCIACICAIGIICAGIGGIGACGIGAGAGAAC 552

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1855 GAACTCAAGGCGTTTGAGGATTCCATGTTTTCCCGCTGGTCTGCTGGTGTGGTTAAGGCC 1914

613 GGATTIGCTGCGCCACTACGTAATTCGGGTG 643

553 ATCCTCGAATCCTTCTCGGATGCGATGTTCGATCGGTGGACTTCCAAACTCGTATCTCTG 612

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us-10-007-527a-1.rni

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; Sequence 19, Application US/09521668B; Patent No. 6303383; Patent No. 6303383; Application; Applicant: NAKANURA, JUN
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US-09-521-668B-19
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Sequence 19, Appl
Sequence 14, Appl
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Sequence 475, Appl
Sequence 81, Appl
Sequence 11, Appl
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Sequence 1202, A
Sequence 15, Appl
Sequence 35, Appl
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Sequence 3664, A
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Sequence 30664, A
Sequence 30664, A
Sequence 30664, A
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Sequence 15639, A
Sequence 14918, A
Sequence 13531, A
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Sequence 1, Appli
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-521-668B-19
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US-09-482-17-81
US-09-482-27-81
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Sequence 17, Application US/0952166BB

Patent No. 6303383

GENERAL INFORMATION

APPLICANT: NAKAMURA, JUN

APPLICANT: KINNO, SOHEI

APPLICANT: KINNO, SOHEI

APPLICANT: MAYAMICA EIICHRO

APPLICANT: MAYAMICA EIICHRO

APPLICANT: MAKAMICO TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA

FILE REFERENCE: 0010-1093-0

CURRENT APPLICATION NUMBER: US/09/521,668B

CURRENT FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 17

LENGTH: 4447
     Sequence 12088, A Sequence 13921, A Sequence 13535, A Sequence 4, Appli Sequence 249, Appli Sequence 249, App Sequence 1299, App Sequence 108, App Sequence 108,
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Sequence 8976, Ap
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Sequence 1, Appli
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53.0%; Pred. No. 0.24;
tive 0; Mismatches 71; Indels 0
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US-09-270-767-12088
US-09-252-991A-13921
US-09-252-991A-13921
US-07-706-699-4
US-07-998-911-4
US-09-902-775A-249
US-09-902-775A-249
US-09-902-775A-249
US-09-902-775A-249
US-09-902-702-249
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Best Local Similarity 53.0
Matches 80; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TISSUE TYPE: Root
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MOLECULE TYPE: DNA (genomic)
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STATE: I.
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APPLICANT: KIMURA, EIICHIRO
APPLICANT: MATSUI, KAUHIRO
APPLICANT: MATSUI, KAUHIRO
ITILE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
FILE REPERENDE: 0010-103-09
CURRENT APPLICATION NUMBER: US/09/521,668B
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: UP 11-69896
PRIOR PILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AACGGCTGGCACGTCCACGTTCACGCGCTACTCATGTTCAGTGGTGACGAGAAC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553 ATCCTCGAATCCTTCTCGGATGCGATGTTCGATCGGTGGACTTCCAAACTCGTATCTCTG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 AATITCTCAAGTTGTTGCTCATCAACTCGGGACTGGATCTGTTGCGATGGTGACGATGAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Syskind, Judith
APPLICANT: Tenatick, John
APPLICANT: Travick, John
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.8; DB 4; Length 1631;
Pred. No. 0.94;
0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1915 GETATGGACGCCCACTGCGTGAGCACGGGG 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATTTGCTGCGCCACTACGTAATTCGGGTG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Brevibacterium lactofermentum
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                                                                                                                                                                                                                                                                                                                                                                                 PatentIn version 3.0
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3.1%;
Best Local Similarity 50.0%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1318)..(2598)
US-09-521-668B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: E. Coli
US-09-492-709A-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-492-709A-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4447
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                                                                                                                                                                                                                                                                                                                                                                                                                        1D NO 19
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                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
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1244 ATTATCACAAGGADAAATGCTCAATTGCTCCTCGAATAATTGAACAGGGCGAACTAT 1303
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                                                                                                                                                                                                                                                                                                                 1304 AGCCCGTGATGAGGCTGTTAAAGATGCGCAACAGAAATCTGCTGAAATTTTCTGC 1357
                                                                                                                                                                                                       339 CATGCGCCATACAGCTGGTCAGCGCCTCCACGACCTATGGACTTTCGGC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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3.0%; Score 34.6; DB 1; Length 1
Best Local Similarity 58.1%; Pred. No. 1;
Matches 61; Conservative 0; Mismatches 44; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,246
FILING DATE: 19920716
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: POCHOPION: 32,167
REGISTRATION NUMBER: 31,167
RECHENCE/DOCKET NUMBER: 91 P 1125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 100: 1:
SEQUENCE CRARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
TOPOLOGY: linear
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us-10-007-527a-1.rni

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537 TGACGIGAGIGAGAGCAICCICGAAICCITCICGGAIGCGAIGTICGAICGGAGGACTIC 596
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CONKIN, Darrell C.
APPLICANT: Yamamoto, Gayle
APPLICANT: Yamamoto, Gayle
APPLICANT: Yamamoto, Gayle
APPLICANT: Gao, Zeren
APPLICANT: Jaspers, Stephen
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG, ZNSSP6
TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG, ZNSSP6
TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG, ZNSSP6
TITLE OF INVENTION ENGER: 000-01-12
PRIOR EPILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AATCACTCACGGAAAAAACGGCTGGCACGTCCACGTTCACGCGCTACTCATGTTCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 TCGTCGTTGGCGTACGGAACGTGAAATGTACGGCTGCGACGGATACGTGCGCGCTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 33.6; DB 3; Length 1134; 30.3%; Pred. No. 1.9; tive 30; Mismatches 110; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lebecque, Serge J.E.
APPLICANT: Liu, Yong-Jun
APPLICANT: Dowling, Lynette M.
APPLICANT: Huffine, Constance M.
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
NUMBER OF SEQUENCES: 6
OTHER INFORMATION: degenerate sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // LOCATION: (1)...(1134)
// OTHER INFORMATION: n = A,T,C or G
US-09-482-180A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mueller, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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LOCATION: (1)...(1134)
OTHER INFORMATION: n is any
NAME/KEY: misc_feature
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Best Local Similarity 30.3%
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                                                                                                           US-09-482-180A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733 GGTAGTGGCGACGGAAAAAGTGGTCGACATGGCAACCGTGCACCCTGGGAAATCGCTGTT 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            913 GAACTAACAGATGCTCAGATCGTTGAGCAGGAAGAA 948
                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29,768
FR: 30472/114 IMMU
                                                                                                                                                                               STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP 91 114 300.6
                                                                                                                                                                                                                                                                                                 COUNTER: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
       Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 8; Conserval
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                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076 cceccacarecageadecereceaadecrecacaceracerecesecaccaaaderec 1133
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Acod, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRNCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LIENGTH: 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                            APPLICALION
FILING DATE: 10-APR-2000
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/813,150
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-82-9196
TELEPHONE: 650-82-9196
TELEPA: 650-82-9106
TELEPHONE: 650-82-9106
TELEPA: 1000 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,553
FILING DATE: 10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 475, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1780 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66..1766
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CRGANISM: Homo Sapien
US-10-140-002-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-09-546-553-3
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US-09-546-553-3

; Sequence 3, Application US/09546553
; Sequence 3, Application US/09546553
; Patent No. 6518405
; Patent No. 6518405
; APPLICANT: Mueller, Christopher
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Lowing, Lymette M.
APPLICANT: Luffine, Constance M.
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: REMAMBLIAN PROTBINASES; OXIDOREDUCTASES;
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Recent
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                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DUS, PAS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 07-MAR-1997
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: SF0693
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 base pairs
TYPR: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
STRY: Palo Alto
STRYE: California
                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; LOCATION: 66..1766
US-08-813-150-3
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REFERENCE/DOCKET NUMBER: 1447-104P
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                                                                                                                                                                                                                                                                                                                                                                                  640 GGTGGTCTCGATGTACGAAAGATCGGCGGTGAAGCTGATCAAGTTCTCGCTGCGTATCTG 699
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                                                                                                                                                                                                                                                                                                     APPLICANT: Thompson, Wayne J.
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Huff, Joel R.
APPLICANT: Bell, Jan M.
TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway Jersey
STRATE: New Jersey
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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DB 4; Length 1844;
                                                                                                                                                                                    53; Indels
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| FACELL NO. 0334031
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: 71 Human Secreted Proteins
| FILE REFERENCE: PZ030P1
| CURRENT APPLICATION NUMBER: US/09/482,273
| CURRENT FILING DATE: 1999-07-14
| EARLIER APPLICATION NUMBER: 60/092,921
| EARLIER FILING DATE: 1998-07-15
| EARLIER APPLICATION NUMBER: 60/092,922
| EARLIER FILING DATE: 1998-07-15
| NUMBER OF SEQ ID NORE: 60/092,956
| EARLIER FILING DATE: 1998-07-15
| NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 33.2; DE Best Local Similarity 55.1%; Pred. No. 3.3; Matches 65; Conservative 0; Mismatches
ch 2.9%; Score 33.2; DI Similarity 55.1%; Pred. No. 3.3; 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/08722001
Patent No. 5760054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Application US/09482273
Patent No. 6534631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA,
ORGANISM: Homo sapiens
US-09-482-273-81
                    Query Match
Best Local Similarity
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778 ACGCACTACTACATCGTCAACCGCTAGTGGCGGTGGCCGACCTCCTGCTCCACCCTCCACGG 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08209747
Patent No. 5733771
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Mir
TITLE OF INVENTION: S11k Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Birch, Stewart, Kolasch
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
                                                                                                                                                                                                                  FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITIA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/POCKET NUMBER: 1916:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1967 base pairs
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NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
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Best Local Similarity
Matches 61; Conserva
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MOLECULE TYPE: CD
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both
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                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-722-001-26
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US-08-209-747-1
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1019 NNNNNNNNNNNNNNNNNNNNNNGGTGCAGGTGCTGGATATGGTGGACAAGGCGGATA 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
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APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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APPLICANT: Dumas Milne Edwards, J.B.
                             28,977
                                                                REFERENCE/DOCKET NUMBER: 14
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                             REGISTRATION NUMBER:
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ORGANISM: Homo sapiens
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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SEQ ID NO 17202
LENGTH: 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708 IGCAICTGGCGTIGGTAGGAGGTIGGTAGTGGCGACGGAAAAAGTGGTCGACATGGCAA 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             899 I'delacticade de la constante de la consta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     768 CCGTGCACCCTGGGAAATCGCTGTTGATGCAGTGGGCGGGGATCCACAAGCGTTGGAACT 827
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Patent No. 5756677
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
ITILE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
ITILE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE BIrch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STREET: Virginia
STAME: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.9%; Score 32.8; DB 1; Length 2793;
39.8%; Pred. No. 5.6;
Ive 0; Mismatches 124; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-UNN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 TGĠTĠĊĊĠĠAĠĊAĠĠAGCTĠĠTĠĊĠĠ 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: minor ampullate gland
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APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUTPBY JF., Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nephila clavipes
                                                 TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.88;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                          LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-209-747-1
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US-08-458-298-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                           918 AACAGATGCTCAGATCGTTGAGCAGGAAGAATCTGCCCCGGTCATGGTTGCGATCATTCC 977
209 RKSSKKCRYSATYYYSCMMKWKKYCMMSATYSGCMMWRWYCYSCMMSRYSCTSYSRGKCS 150
                                                   858 ACGICGGGCAATCGCGTGGTCCCGTGGATTGCGTGCCCGAGCTGGTCTTGGGGCAGAACT 917
                                                                            Gaps
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2.9%; Score 32.6; DB 4; Length 1431;
Best Local Similarity 49.7%; Pred. No. 4.5;
Matches 83; Conservative 0; Mismatches 84; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
                                                                                                                                                                                                       978 GGCGCGATCGTGGATGATCGGACTT 1006
                                                                                                                                                                                                                            29 MGKCSRCTCCMGGCGGYTYCMKSCSRYYT 1
                                                                                                                                                                                                                                                                                             RESULT 15
US-09-614-912-49/c
; Sequence 49, Application US/09614912
...ar No. 6677502
                                                                                                                                                                                                                                                                                                                                                                                       Allen, Steve
Rafalski, Antoni
Oroco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Caimi, Perry G
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LOCATION: (1309)
NAME/KEY: unsure
LOCATION: (1339)
NAME/KEY: unsure
LOCATION: (1313)
NAME/KEY: unsure
LOCATION: (1402)
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; NAME/KEY: unsure
; LOCATION: (1429)
US-09-614-912-49
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SEQ ID NO 49
LENGTH: 1431
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APPLICANT:
APPLICANT:
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850 GCGCCCGGCGGGGCCTGATGGAGCGCCACGCGAGCGTGGCGGCGCTCGAACACCTGGAGT 791

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Oy 950 CTGCCCGGTCATGGTTGCGGCGCGATCGTGGATGATGTGTTGTG 1009

Db 790 CGCCCCGGTCATGGTGTGAGGTGAGGGGGGGTCGTGATTCGGCCCCGTG 731

Qy 1010 CGCCTTACGTCTTCGGCGAGATCCTCGGACTCGTGAGGGGG 1056

Db 730 CCCAGCGTGTTCGGCGAGATCCTCGGAGTGGTGG 684

Search completed: October 23, 2004, 02:20:26

Job time: 129 secs
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October 23, 2004, 01:10:16; Search time 618 Seconds (without alignments) 9451.893 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7 NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7 NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3407233 segs, 2561960514 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0 , Gapext 1.0
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1140
                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES		
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No.	Score	Match	Match Length DB	DB	ΙD	Description	
	1140	100.0	:	14	US-10-007-527A-1	Segmence 1. 7	Appli
2	1140	100.0		14	US-10-007-452-1	Sequence 1. 7	Appli
3	1140	100.0	1140	17	US-10-415-562A-1	Sequence 1. 7	Appli
O 4	1140	100.0		14	US-10-007-527A-5	Sequence 5. 7	Appli
O S	1140	100.0		14	US-10-007-452-5	Sequence 5. 7	Appli
9 0	1140	100.0		17	US-10-415-562A-5		Appli
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c 12	1140	100.0	11241	17	US-10-415-562A-6	. 9	Appli

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3.3 4447 9 3.3 4447 15 3.2 299 14 3.2 299 14 3.2 299 14 3.2 299 14 3.2 2560 16 3.1 498 16 3.1 498 16 3.1 601 19 3.1 1631 9	лышшышшышшышшы йышшааааааннчно			
3.3 4447 9 3.3 4447 15 3.2 299 14 3.2 299 14 3.2 299 14 3.2 299 14 3.2 2560 16 3.1 498 16 3.1 498 16 3.1 601 19 3.1 1631 9	6.00.00.00.00.00.00.00.00.00.00.00.00.00			88888888888888888888888888888888888888

ALIGNMENTS

	0;	09	120
Vectors	Length 1140; Indels 0; Gaps	ATGACCAGCGTAAGTGCTGAACACCTTTCCGGCAAAGACCGGCCTCCCGTCTCGTGTCG 6	TCCGATAAGGGGGGCATCGGGACGGAACTGCGACCCAAACTTCAACAAATGACCAGGTCA 1
and Expression	DB 14;	CGGCAAAGACCGGC CGGCAAAGACCGGC	GCGACCCAAACTTC GCGACCCAAACTTC
10007527A 10015 10015 10015 10015 10016 10017 10	100.0%; Score 1140; 100.0%; Pred. No. 0; ive 0; Mismatches	GCTGAACACCTTTC GCTGAACACCTTTC	ATCCGGCACGAACT
SULT 110-007-527A-1 Subjuction US/10007527A Subjuction US/0007527A Subjuction US. US2033044807A1 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Tomb, Jean-Francois APPLICANT: Cheng, Qiong APPLICANT: Cheng, Qiong APPLICANT: Cheng, Qiong APPLICANT: Cheng, Ciong APPLICANT: Cheng, Usong APPLICANT: Cheng, Usong APPLICANT: Cheng, Oiong APPLICANT: APPLICATION NUMBER: US10/007,527A CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Microsoft Office 97 LENGTH: 1140 TYPE: DNA ORGANISM: Rhodococcus AN12	ilarity Conservat	atgaccagcgtaagi 	
RESULT 1 US-10-007-527A-1 Sequence 1, Applicat Publication No. US20 GENERAL INFORMATION: APPLICANT: Tomb, Jo- APPLICANT: Cheng, APPLICANT: Cheng, APPLICANT: Cheng, APPLICANT: Cheng, APPLICANT: ROSTICH TITLE OF INVENTION: FILE REFERENCE: CL1 CURRENT FILING DATE PRIOR APPLICATION N PRIOR FILING DATE; NUMBER OF SEQ ID NO SOFTWARE: MICROSOFE; SEQ ID NO 1 LENGTH: 1140 LENGTH: 1140 LYPE: DNA CRGANISM: Rhodococ US-10-007-527A-1	Query Match Best Local Similarity Matches 1140; Conserv	Qy 1 Db 1	Qy 61 Db 61

721 GGTATGGAGGTTGGTAGTGGCGACGGAAAAGTGGTCGACATGGCAACCGTGCACCTGG 780

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RESULT 2 US-10-007-452-1 Sequence 1, Application US/10007452 ; Publication No. US20030093701A1

Db 301 CAACTCGGGACTGGATGTGGCGATGACGATGCGCCATGCGCCCGG 360	721 GGTATTGGTAGTTGGTAGAAAAAGTGGTGGTATCTGACGAAAATTGCATCTGGCGTTT 721 GGTATTGGTAGTTGGTAGTGGAAAAAGTGGTCGAAAAAGTGGTCGAAAAAGTGGTCGAAAAAGTGGTCGAAAAAGTGGTCGAAAAAGTGGTCGAAAAGTGGTCGAAACGTGGAAACCGTGCACCCTGG 721 GGTATTGGGTTGGTGGTGGGCGAAAAGTGGTCGAATTGGTGGCGAGAATTT 731 GAAATCGCTGTTGATGCAGTGGGCGAACCCAAGCGTTGGAACTGTGGCGAGAATTT 731 GAAATCGCTGTTGATGCAGTGGGCGAGGAATCCACAAGCGTTGGAACTGTGGCGAGAATTT 841 GAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTCCCGTGGATTGGCTGCCCGAGCT 841 GAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTCCCGTGGATTGCGTGCCCGGGCG 841 GAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTTCGAATTGCGTCCCGGGCC 841 GAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTTCGAATTGCGTCCCCGGGC 901 GGTCTTGGGGCAAACAACAAGATGCTCAAATCGTTGAGCATGCCCCGGTC 902 GGTCTTGGGGCAAACAACAAGATGCTCAAATCGTTGAGCATGCCCCGGTC 903 GGTCTTGGGGCAAAACAAACAAGATGCTCAAATCGTTGAGCATGCTCCCCGGTC 91 ATGGTTGCCAAACAACAACAATCGTCGAATCGTTGAGCATTGTGCGCCTTAACGTC 91 ATGGTTGCCAATCAATCAATGATGATTGTTCGGACCTTAACGTTCTAATGATTGTTCGAATCTTGTCCCCCGGTC 91 ATGGTTGCCAATCGTCGAATCGTTCAATGATTGTTCGAACTTTATGGCTTTAACGTTCTAATGATTTCTAATGATTGTTCTAATGATTTTTTTT	OY 1021 TTCGGCGAGATCCTCGGACTCGTCGAAGCTTCGGAAAATCTTCGTGATCA 1020 Db 1021 TTCGGCGAGATCCTCGGACTCGTCGAAGCTTCGGAAAATCTTCGTGATCA 1080 OY 1081 TTCGACTATATCGATTCGTCGTCGAAGCTTGGGAAAATCTTCTGTGATCAC 1080 OY 1081 TTGCATTATCGATTGCTCGCGCGATGTGCGGCCCCCGATAATATCGGTTCGTGATCAC 1140 RESULT 4 US-10-007-527A-5/c ; Sequence 5, Application US/10007527A ; Publication No. US20030044807A1 ; GENERAL INFORMATION: APPLICANT: Tomb, Jean-Francois APPLICANT: Chang, Qiong APPLICANT: APPLICATION NUMBER: US/10/007,527A FILE REFERENCE: CL1709 US NA CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 30 SOFTMARE: Microsoft Office 97 SEQ ID NO 5
Db 721 GGTATGGAGGTTGGTAGTGGCGAAAAAGTCGTCGACATGCCAACCGTGCACCCTGG 780	RESULT 3 US-10-415-562A-1 Sequence 1, Application US/10415562A Sequence 1, Application US/10415562A Publication No. US20040115661A1 GENERAL INFORMATION: APPLICANT: E.I. du Pont De Nemours and Company TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors CURRENT APPLICATION NUMBER: US/10/415,562A CURRENT APPLICATION NUMBER: US/10/415,562A PRIOR FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Microsoft Office 97 SEQ ID NO 1 LENGTH: 1140 TYPE: DNA ORGANISM: Rhodococcus AN12 US-10-415-562A-1	Query Match 100.0%; Score 1140; DB 17; Length 1140; Best Local Similarity 100.0%; Pred. No. 0; N. Simatches 0; Indels 0; Gaps 0; ATGACCAGGGTAAGTGCTGAACACTTCCGGCAAAGACCGCCTCCTCGTGTCG 0 1 ATGACCAGGGTAAGTGCTGAACACTTCCGGCAAAGACCGCCTCCTCGTGTCG 60 Db 1 ATGACCAGGGTACGACCAACACTTCCGGCAAAGACCCCCTCCTCGTGTCG 60 CV 61 TCCGATAAGCGCGACCAACACTTCCGGCAAACTTCAACAAATCACCACGTCA 120 Db 61 TCCGATAAGCGCGCACCAACATTCGGCCTCAACATTCAACACCACGTCA 120 CV 121 GAAACATTTAACGCCTGGACCGACCAACTTCGGCGTGAACGTGTAACACCACGTCA 120 Db 121 GAAACATTTAACGCCTGGCCGACCAATTCTGGCGTGAACGGTGTAACACTTCTCACCACGTCA 120 CV 121 GAAACATTTAACGCCTGTGGCGGATTTCTGGCGTGAACGGTGGATTGTCCCC 240 Db 121 GAAACATTTAACGCCTGTGGCGGATTTCTGGCGGAACGGTGGATTGTCCCC 240 CV 181 GGTCCGAAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAACGGTGGATCTGCCCC 240 CV 181 GGTCCGAAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAACGGTGGATCTGCTCC CV 181 GGTCCGAAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAACGGTGGATCTGCTCATTGCTCC CV 181 GGTCCGAAAGGTTCTGGATTCGTCCTCGCGGAAACGGTGGATTGCTCCTCATTGCTCCTCATTGCTCCC CV 181 GGTCCGAAAGGTTCTGGATGCACCATTCTCTCTCGCGGAAACGGTCGATTGCTCCTCATTGCTCCC CV 181 GGTCCGAAAGGTTCTGGCGAAACGGTGGAACGGTGGATTGTTCTCATTGCTCCC CV 181 GGTCCGAAAGGTTCTGCTCGCGGAAACGGTGA

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481 ACTCACGGAAAAACGGCTGGCACGTCCACGTTCACGCGCTACTCATGTTCAGTGGTGAC 540
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AIGGIIGCGAICAITCCGCCGCGAICCIGGAICAIGAICACAICGGACIIGIGCGCCTIACGIC
            2091 AIGSTIGCGAICCITCCGGCGCGAICGIGGAIGAITCGGACTIGIGCCTTACGIC
                                                                TIGCATTAICGATTGCCCGCAGCGGATGTGCGCCCCCCGATAATATCGGTTCGCAAGTGA
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; Sequence 5, Application US/10007452
; Publication No. US20030093701A1
; GENERAL INFORMATION:
    APPLICANT: Tomb, Jean-Francois
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Cheng, Qiong
; APPLICANT: Cheng, Qiong
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Rhodecoccus Cloning and Expression Vectors
; TITLE OF INVENTION: Rhodecoccus (2007)
; TITLE OF INVENTION: Rhodecoccus (2007)
; TITLE OF INVENTION NUMBER: 60/254,868
; PRIOR APPLICATION NUMBER: 60/254,868
; PRIOR FILING DATE: 2000-12-12
; RRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NOS: 30
; SEQ ID NO 5: 30
; SEQ ID NO 5: 30
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; ORGANISM: Rhodococcus AN12
US-10-007-452-5
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IIILE OF INVENTION: Rhodococcus Cloning and Expression Vectors
FILE REFERENCE: CL1709 US PCT
CURRENT APPLICATION NUMBER: US/10/415,562A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO S.
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; Sequence 7, Application US/10007452
; Publication No. US2030093701A1
; GENERAL INFORMATION:
    APPLICANT: Tomb, Jean-Francois
; APPLICANT: Cheng, Qiong
; APPLICANT: Cheng, Qiong
; APPLICANT: Cheng, Qiong
; PILE REFERENCE: CL1709 US NA
; TITLE OF INVENTION NUMBER: US/10/007, 452
; CURRENT APPLICATION NUMBER: 60/254, 868
; PRIOR APPLICATION NUMBER: 60/254, 868
; PRIOR PILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 30
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Best Local Similarity 100.
Matches 1140; Conservative
                                                               TYPE: DNA
ORGANISM: Plasmid pRHBR17
   NOS:
NUMBER OF SEQ ID NOS
SOFTWARE: Microsoft
SEQ ID NO 7
                                               LENGTH: 9652
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US-10-415-562A-7
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Publication No. US20040115661A1
GENERAL INFORMATION:
APPLICANT: B.1. du Pont De Nemours and Company
TITLE OP INVENTION: Rhodococcus Cloning and Expression Vectors
FILE REFERENCE: CL1709 US PCT
CURRENT APPLICATION NUMBER: US/10/415,562A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR FILING DATE: 2000-12-12
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| Sequence 6, Application US/10007452|
| Publication No. US20030093701A1 |
| Publication No. US20030093701A1 |
| GENERAL INFORMATION: |
| APPLICANT: Tomb, Jean-Francois |
| APPLICANT: Chemic, Michael G. |
| FILE OF INVENTION: Rhodococus Cloning and Expression Vectors |
| FILE REFERENCE: CL1709 US NA |
| CURRENT FILING DATE: 2001-11-08 |
| PRIOR FILING DATE: 2001-11-08 |
| PRIOR FILING DATE: 2001-12-12 |
| NUMBER OF SEQ ID NOS: 30 |
| SOFTWARE: Microsoft Office 97 |
| FEMALET OFFICE 
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Best Local Similarity 100.
Matches 1140; Conservative
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US-10-007-452-6
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4152 GETCTTGGGGCAGAACTAACAGATGCTCAGATCGTTGAGCAGGAAGAATCTGCCCCGGTC
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US-10-007-527A-6/c

i Sequence 6, Application US/10007527A

i Publication No. US20030044807A1

i GENERAL INFORMATION:

APPLICANT: Tomb, Joan-Francois

APPLICANT: Cheng, Qiong

APPLICANT: Kostichka, Kristy N.

TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors

FILE REFERENCE: CLily09 US NA

CURRENT APPLICATION NUMBER: US/10/007,527A

CURRENT APPLICATION NUMBER: 60/254,868

FRIOR APPLICATION DATE: 2000-12-12

PRIOR PILING DATE: 2000-12-12
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100.0%; Score 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1140; Conservative 0; Mismatches
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SOFTWARE: Microsoft Office 97
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CCTATGACTGACTTTCGGCACCTGGAAAGCTGCGACCAACGGTCGT 420 CCTATGACTTTCGGCACCTGGAAAGCTGCGACCAACGGTCGT 6222 GGAACGTGAAATTCGGCACCTGGAAAGCTGCGCACCAACGGTCCT 6222 GGAACGTGAAATTCGGCACCTGCACCAATACTGCGCCCTGTTGAAATC 6162 AAACGGCTGGCACCTTCACGCGCACCTGTTCAAATC 6102 AAACGGCTGGCACCTTCACGCGCTGTTCCAATGGTCCACCTGTTCAAATC 6102 AAACGGCTGGCACTTCACGCGCTCTCATGTTCAGTGGTCAC 6102 AAACGGCTGGCACTTCACGCGTCTCCATGTTCAGTGGTCAA 600 CATCCTCCAATTCCTTCTCTGCTTCATCTCATGTTCAGTGGTCAA 600 CATCCTCCAATTCCTTCTTCAGTTCAGTCGATTCCATGTTCAAAA 600 CATCCTCCAATTCCTTCTTCAGTTCATCTCATGTTCAAAA 600 CATCCTTCTTCTTCTTCTTCTTCTTCATTCTATTCATTC	AACTC	STCAG	; ; ; US-1	LENGIR: 11441 TYPE: DNA ORGANISM: Plasmid pRHBR17 10-415-562A-6
	CGGCT	310GT	A B O	100.0%; Score 1140; DB 17; Length 11241; 100.0%; Pred. No. 0; Ative 0; Mismatches 0; Indels 0;
AAACGGCTGGCACGTCCACGTTCACGCGCTACTTCACGGGTGAC 540 AAACGGCTCGCACGTCCACGTTCACGCGCTACTTCATGGTGAC AAACGGCTCGCACGTCCACGTTCACGCGCTACTCATGGTGAC AAACGGCTCGCACGTCCACGTTCACGCGCTACTCCATGGTGAC CATCCTCGAATCCTTCTCGCATGTTCCATCGTCTCCAAA 600 CATCCTCGAATCCTTCTCGCATGTTCCATCGTCCAAAC 600 CATCCTCGAATCCTTCTCCGATGCTTCCATCGTCCAAAC 600 CATCCTCGAATCCTTCTCCGATGTTCCATCGTCTCCAAAC 600 CATCCTCGAATCCTTCTCCGATGTTCCATCGTCTCCAAAC 5802 CATCCTCGAATCCTTCTCCCATCTTCCATCGTCTTCCAAAC 5802 CATCCTCAATCAATTCCTCCCTCCATCTTCCAAACTTCCCATCTTCCAAACTTCCCAAAC 5802 CATCCTCAATCAAGTTCTCCCTTCCATCTCCAAAATTCCATCTCCAACTTCCCAAAC 5802 CATCCTCAATCAAGTTCTCCCTTCCAAAATTCCATCTCCAACTTCCAACTTCCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAAATTTCCATCCACCTCCAAACTTCAAAAATTTCCAAAATTTTTT	CGTTG CGTTG	AAATC	& a	1 AIGACCAGGGTAAGTGCTGAACACCTTTCCGGCAAAGACCGGCCTCCCGTCTCGTGTCG 60
CATCCTCGAATCCTTCTCGGATGCATTCGATCGATCGACTTCCAAA 600 CATCCTCGAATCCTTCTCGGATGCATTCGATCGATGGACTTCCAAA 6042 CATCCTCGAATCCTTCTCGGATGCTTCGATGGACTTCCAAA 6042 CATCCTCGAATCCTTCTCGGATGCTTCGATGGATGGATTCCGAAAG 5982 GGGATTTGCTGCGCCACTACGTAATTCGGGTGGTCTCCAAAG 5982 GGGATTTGCTGCGCCACTACGTAATTCGGGTGGTCTCCAAAG 5982 CACCGATCAACAACACTCTCGAAAATTCGATCTCGAAAG 5982 CACCGATCAACAACACTCTCGCTGCACAAAATTCCATCTCGCGGTT 720 CACCGATCAACAACTCTCGCTGCACAAAATTCCATCTCGCGGTT 720 CACCGATCAACAACACTCCCACAAAATTCCATCTCGCCGCTT 720 CACCGATCAACAACACTCCCACAAAATTCCATCGCCCCCTCG 780 CACCGATCACCCCACAAAAATTCCACTCGCACACCCTCG 5862 CACCGATCACCCCACAACACCTTCGACACACCCTCGAATTT 5802 CACCGAACTCACCACACACCCTCGAATTCTCGCCCCACACCTT 590 CACCGAACTACACACACCCTCGAATTCCCCCCCACCCTCGAATTT 5802 CACCGAACTACACACACCCTCGAATTCTCGCCCCCACCCTCGAATTT 5802 CACCCCACACACACACCCTCGAATTCTCGCCCCCACCCTCGAATTT 5802 CACCCCACACACACACCCTCGAATTCTCGCCCCCACCCCTCGAATTT 5802 CACCCCACACACACACACACACACACACACACACACAC	ACTCA ACTCA	STGAC STGAC	ò a	
	TGAG IGAG	CCAAA	Sp Sy	121 GAAACATTDAACGCCTGTGGCCGGCGGTTTCTGGCGTGAACGGTGTGACCATTGTCAAC 180
	TCGT 	SAAAG SAAAG	ò da	181 GGTCCGAAGGTTCTGGATTCGGAGGCCTTCGTTCCTGCGGAAAGGGCTGGATCTGCCCC 240
	ATCGG	GGTGAAGCTGATCAAGTTCTCGCTGCGTATCTGACGAAAATTGCATCTGGCGTT 	λ δ	
	GTAT 3TAT	CCTGG	ờ a	
GATGGGACATCGGCATCGCTGCATTGCGTGCCCGAGCT 900 QY 421 GATGGGACATCGCGTGGTCCCGTGGATTGCGTGCCCGAGCT 5742 Db 6221 GATGGGACGTCGGTGGTCCCGTGGATTGCGTCCCGGTC 960 QY 481 AGAACTAACAGATGGTGAGAATCTGCCCCGGTC 560 QY 481 AGAACTCAGATGGTGAGAATCTGCCCCGGTC 562 Db 6161 AGAACTAACAGATGGTGAGAATCTGGCCCTTACGTC 562 Db 6161 CATTCCGGCGCAATCGTGAATGATTGGCCCTTACGTC 5622 Db 6101 CATTCCGGCCGAATCGTGGACTTGGGAATTGTCGCCCTTACGTC 5622 Db 6101 CCTCGGACTCGTGAAGCTGGCGGACTTGGGAAATCTTCGTGAATCAC 1080 QY 601 CCTCGGACTCGTCGAAGCTGGCGGACTTGGGAAAATCTTCGTGAATCAC 1080 QY 601 CCTCGGACTCGTCGAAGCTGGCGCACTTGGGAAAATCTTCGTGAATCAC 1080 Db 601	GAAATO GAAATO	GCTGTTGATGCAGTGGGGGGGATCCACAAGCGTTGGAACTGTGGGCGAGAATTT 	b Q	
CGGTC 960 Qy 481 CGGTC 5682 Db 6161 CGGTC 1020 Qy 541 ACGTC 5622 Db 6101 ACGTC 1080 Qy 601 ACGTC 5522 Db 601 ACGTC 5522 Db 601 ACGTC 5522 Db 601	AGTT AGTT	GATGGGACGTCGGCAATCGCGTGGTCCCGTGGATTGCGTGCCCGAGCT	ko aa	
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ATCAC 1080 QY 601	1661 	ACGIC ACGIC	y d	
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Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 74; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCOUNTS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT PILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                 ATCGGCGTGAAGCTGAAGTTCTCGCTGCGTATCTGACGAAAATTGCATCTGGCGTT
                                                                 GGTATGGAGGTTGGTGGCGACGGAAAAAGTGGTCGACATGGCAACCGTGCACCCTGG
                                                                                                                                  GAAATCGCTGTTGATGCAGTGGGGGGGGATCCACAAGCGTTGGAACTGTGGCGAGAATTT
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ATCGGCGGTGAAGCTGATCAAGTTCTCGCTGCGTATCTGACGAAAATTGCATCTGGCGTT
                                                                                                                                                                                                   GAGTTTGGTTCGATGGGACGTCGGCCAATCGCGTGGTCCCCGTGGATTGCGTGCCCGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 332, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godward; Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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US-10-184-644-332
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                             210 QGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGWKGDAGV
                                                                                                                                           270 MGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQGQPGLQGVPGPPGAVGHPGAKGEPGSAGS
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APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Watenabe, Colin K.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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al Similarity 18.5%; Pred. No. 0.018;
74; Conservative 81; Mismatches 246;
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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US-10-184-634-332
; Sequence 332, Application US/10184634
; Publication No. US20030066684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
ropi.ICANT: Chen, Jan
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330 PGRAGLPGSPGSPGATGLKGSKGDTGLQGQQGRKGESGVPGPAGVKGEQGSPGLAGPKGA 389
                                                                            990 PGQAGQKGDQGVKGSSGGQGVKGEKGEKGERGENSVSVRIVGSSNRGRAEVYYSGTWGTICDD 449
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                                               822 GGAACTGTGGCGAGAATTTGAGTTTGGTTCGATGGGACGTCGGGCAATCGCGTGGTCCCG 881
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICATE: Signal Tau Industrie Farmaceutiche Riunite S.P.A. TITLE OF INVENTION: Long Pentaxin PTX3 and Female Sterility FILE REFERENCE: 012-27-01-02 CURRENT APPLICATION NUMBER: US/10/485,640 CURRENT FILING DATE: 2004-02-03 PRIOR PPLICATION NUMBER: US 60/309,472 PRIOR PELICATION NUMBER: US 60/309,472 NUMBER OF SEQ ID NOS: 11 SOFTWARE: PATENTIAN PATE: 2001-08-03 SEQ ID NOS: 11 LENGTHA: 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.6%; Score 40.6; DB 18; Length 1
Best Local Similarity 48.5%; Pred. No. 0.035;
Matches 112; Conservative 0; Mismatches 119; Indels
                                                                                                                                              882 TGGATTGCGTGCCCGAGCTGGTCTTGGGGCAGAACTAACAG 922
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Job time : 621 secs
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PAGES: 1862-1872
DATE: 1996-03-01
DATABASE ACCESSION NUMBER: X83601
DATABASE ENTRY DATE: 1996-01-10
                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/10485640; Publication No. US20040198655A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Introna et al.
TITLE: Cloning of Mouse PTX3
JOURNAL: Blood
VOLUME: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                        RESULT 15
US-10-485-640-3
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein October 23, 2004, 02:18:21; Search time 85 Seconds (without alignments) 1599.511 Million cell updates/sec Run on:

US-10-007-527A-2 2005 1 MTSVSAEHLSGKDRPPVLVS.........HLHYRLPAADVRPPIISVRK 379 score: Sequence: Title: Perfect

2002273 segs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

2002273 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

STIMMARTES

	Description	842	Abb84280 A. pyogen	Aaw73071 B. breve	Aay97536 B. lactof	Abb06341 Brevibact	Aae13530 B. lactof		m m	Abb06342 Brevibact	Aae13531 B. lactof		Н	Aaul1039 Replicati	Abb84282 S. phaeoc	Aap93143 Sequence		Abu56572 Lung canc	Abo68907 Pseudomon	Abo81599 Pseudomon	Aaw06554 R. capsul	Abg03109 Novel hum	Abo74435 Pseudomon	Abu15733 Protein e	Abo70485 Pseudomon	Abo73536 Pseudomon
SUMMARIES	ΩI	ABB84	ABB84280	AAW73071	AAY97536	ABB06341	AAE13530	ABB84283	AAY97537	ABB06342	AAE13531	ADB66179	ABB84281	AAU11039	ABB84282	AAP93143	AAE37298	ABU56572	ABO68907	ABO81599	AAW06554	ABG03109	ABO74435	ABU15733	ABO70485	AB073536
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ď	Query Match	100.0	30.4	19.9	16.3	16.3	16.3	16.1	15.9	15.9	15.9	15.9	15.8	14.1	13.3	6.7	5.2	5.1	5.1	5.0	5.0		5.0	4.9	4.9	4.9
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Adk16042 Streptomy	Abo82189 Pseudomon	Aay58582 Sorangium	Abo76754 Pseudomon	Abo63712 Klebsiell	Abo82117 Pseudomon	Aay58577 Sorangium	Aae36999 Micromono	Adh41829 Novel hum	Abo82636 Pseudomon	Abp65883 Bifidobac	Aaw52847 A. medite	Aae30185 Human PHD	Abo73550 Pseudomon	Adm26351 Hyperther	Aao24108 Synechoco	Abb10262 Human cDN	App66849 Human pol	Abo62802 Klebsiell	Abr41258 Human DIT
ADK16042	AB082189	AAY58582	AB076754	AB063712	AB082117	AAY58577	AAE36999	ADH41829	AB082636	ABP65883	AAW52847	AAE30185	AB073550	ADM26351	AA024108	ABB10262	ABP66849	AB062802	ABR41258
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98.5	97.5	97	97	96.5	95.5	95.5	95.5	94.5	94.5	94.5	94.5	94	94	94	94	93.5	93.5	93.5	93.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Rhodococcus AN12 replication protein Rep. ABB84278 standard; protein; 379 AA. (first entry) 13-JAN-2003 ABB84278; RESULT 1 ABB84278

Plasmid stability protein; replication protein; ethylene forming enzyme; carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase; polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dahydrogenase; terpene synthase; cholesterol oxidase; shuttle vector; Rep protein.

Rhodococcus erythropolis.

WO200255709-A2.

18-JUL-2002

12-DEC-2001; 2001WO-US047868.

12-DEC-2000; 2000US-0254868P.

Е Н (DUPO) DU PONT DE NEMOURS & CO

Tomb J; Kostichka KN, Cheng Q, Bramucci MG,

WPI; 2002-557827/59.

N-PSDB; ABQ76122.

New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.

Claim 4; Page 64-65; 96pp; English.

This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isopremoid molecules, polyhydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile hydrateases, ethylene forming enzyme, pyruvate decarboxylase, alcohol dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in

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97JP-00091387.
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Best Local Similarity 36.33
Matches 148; Conservative
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                                                                                                                                                                          Sequence 459 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle
shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents the Rhodococcus AN12 Rep protein described in the disclosure of the invention
                                                                                                                                                                                                                                                                                GMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQALELWREFEFGSWGRRAIAWSRGLRARA
                                                                                                                GPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTGSVAMVTMTMRHTAGQ
                                                                                                                                                                                   RLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGD
                                                                                                                                                                                                                                        GLGAELTDAQIVEQEESAPVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDH
                                                                                                   MTSVSAEHLSGKDRPPVLVSSDKRGIRHELRPKLQQITTSETFNACGRPISGVNGVTIVN
                                                                                                                                                                                                       RLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGD
                                                                                                                                                                                                                                                                   GMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQALELWREFEFGSMGRRAIAWSRGLRARA
                                                                                                                                                                                                                                                                                                          GLGAELTDAQIVEQEESAPVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDH
                                                                                                                                                                                                                           VSENILESFSDAMFDRWTSKLVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLTKIASGV
                                                                                 Gaps
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                                                             Length 379;
                                                                                Indels
                                                          100.0%; Score 2005; DB 5;
100.0%; Pred. No. 6.6e-193;
ive 0; Mismatches 0;
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                                                                               Matches 379; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-557827/59
                                                                     Local Similarity
                                        Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shuttle vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-----DVRKIGGEADQVLAAYLTKI---ASGVGMEVGSGDGKSGRHGNRAPWEIAVDA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isoprenoid molecules, polyhydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile dehydraceases, ethylene forming enzyme, pyruvate decarboxylase, alochol dehydraceases, terpene synthases, and cholesterol oxidase in an Actinomyceases bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents A. pyogenes pAPI replication protein described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VG-GDPQALELWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQIVEQEESAPVMVAII 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 RAKSDGKGAGYGGLHTCGSVWACPVCSAKIAARRKTDLQQVVDHAVKHGMTVSMLTLTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 IIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTG-SVAMVTMTMR
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for expression of heterologous genes in Rhodococcus species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 609.5; DB 5;
Pred. No. 3.5e-52;
2; Mismatches 133;
                                                         5; Fig 4A; 96pp; English.
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36.3%; Pre-
tive 62; ]
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Corynebacterium glutamicum.
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                                                                                                                                         Shuttle vector for a Bifidobacterium species - contains specific elements from existing plasmids e.g. pNBb1 of ATCC 15698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 NHAEKLRKAAADOWQAEHEGQRLPPELMVSDSFGNYIFGTLTLRHDRTMPLAMTLDAILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.9%; Score 399.5; DB 2; 27.2%; Pred. No. 5.6e-31; ive 64; Mismatches 169;
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                                                                                                                                                                                                                 Claim 5; Page 14-15; 17pp; Japanese
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VSAEHLSG-KDRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116; Conservative
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                      (HONS ) YAKULT HONSHA
                                                                     WPI; 1998-587288/50.
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Best Local Similarity
                                                                                              N-PSDB; AAV58945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 494 AA;
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This sequence is the Brevibacterium lactofermentum p48K protein. The invention relates to a plasmid containing a temperature sensitive caplication control region (FSRCR) and a marker gene (MG). The TSRCR is derived from plasmid pAM30 harboured by Brevibacterium lactofermentum (ATCC 13869) and allows the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. The plasmid can be used for the chromosomal gene in a coryneform bacterium, which may be used for the production of useful substances, such as amino acids, by fermentation, to change their genetic traits. Therefore, the plasmid can be used for breading microorganisms for the production of amino acids by fermentation. The plasmid comprises a TSRCR that allows the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. (Updated on 12 -SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmids containing a temperature sensitive replication control regions useful for breeding microorganisms for the production of amino acids by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 GMDAPLREHGVKLDQVSTWGGDAAK-MATYLAK---GMSQELTGSATKTASKGSYTPFQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LOQITTSETFNACGR-----PISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKV
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                                                                                                                                                                                                                                 Nakamatsu
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                                                                                                                                                                                                                              Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 14-17; 29pp; English.
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                                                                                                                                                                                                                              Kimura
                                                                           99JP-00069896
16-MAR-2000; 2000EP-00105326
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Best Local Similarity 29.15
Matches 98; Conservative
                                                                                                                                                  (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                              Kanno S,
                                                                                                                                                                                                                                                                                                     2000-573832/54.
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                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA90934
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                                                                           16-MAR-1999;
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98 79 204

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The present invention describes a method for transforming a high temperature-resistant coryneform microbe in which the high temperature-resistant coryneform microbe and an electric pulse is applied to structure of cell wall of the microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall of a middle microbe in which the cell wall of a high temperature-resistant coryneform microbe in which the cell wall of a high temperature resistant coryneform microbe having weakened cell wall and a DNA; (2) a transformant of a high temperature-resistant coryneform microbe having weakened cell wall and a DNA; (2) a transformant of a high temperature-resistant coryneform microbe and (3) a transformant of a high temperature-resistant coryneform microbe and coryneform microbe in which a recombinant DNA is introduced; and (3) a transformant of a high temperature- resistant coryneform microbe and a chieved from the high temperature- resistant coryneform microbe and a chievefermentum. The method is used for transforming a high temperature-coryneform microbe. The present sequence represents a Brevibacterium lactofermentum pSFK6 protein sequence, which is used in an example from the present invention. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |:: | : | | : : |:| | 30 MGERRIELAIATKNHIAAAGGAIMMFVGTVRHNRSQSFAQVEAGIKTAYSSMVKTSQWKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 GAHRADEISQVVAHQLGTGSVAMVTM-TMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformation of high temperature-resistant coryneform microbe and
                                                                                                                                                                                                                                           Brevibacterium lactofermentum pSFK6 protein sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                               high temperature resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                               mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 18-19; 28pp; Japanese
ABB06341 standard; protein; 427 AA.
                                                                                                                                                                                                                                                                                                                  gene; mutation transformation
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                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum.
                                                                                                                                                                           (first entry)
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                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AJIN ) AJINOMOTO KK.
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                                                                                                                                                                                                                                                                                                           Kanamycin resistant
coryneform microbe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL49733
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                                                                                                                                       29-AUG-2003
29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2002
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                                                                   ABB06341;
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The present invention relates to Coryneform bacterium in which the arginine repressor does not function normally and which produces Larginine. Coryneform bacterium is used to produce L-arginine which is useful in agents for promoting liver function and in amino acid infusions or in 'comprehensive' amino acid pharmaceutical. Coryneform bacterium accumulate L-arginine to higher levels than wild-type strains, e.g. 120 compared with 20, mg/dl. The present sequence is Brevibacterium lactofermentum pSFK6 replication control region protein. The replication control region bNA is used in the construction of fauttle vector for Escherichia coli and Coryneform bacteria and temperature sensitive vector. (Updated on 29-AUG-2003 to standardise OS field)
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                    -- LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQI--- 311
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                                                                                                                                                                                                                                                                                                                        Coryneform bacteria; arginine repressor; L-arginine; liver function; amino acid infusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium with inactivated arginine repressor, useful for fermentative production of arginine at high levels.
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                                                                                                                                                                                                                                                                                                   B. lactofermentum pSFK6 replication control region protein.
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29.1%; Pred. No. 1.2e-23;
cive 58; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                     (first entry)
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16.3
Best Local Similarity 29.1
Matches 98, Conservative
 263 AVDAVGGDPQALE-
                                                                                                                                                                                                                                                     (revised)
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                                                                    312 VEQE
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12-FEB-2002
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146 REMYGCDGYVRAVEITHG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSL 204

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263 AVDAVGGDPQALE-----LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAOI--- 311
                                                                                                                                        This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of septembolical enclass, polyhydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile hydrateses, ethylene forming enzyme, pyruvate decarboxylase, alchol dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents the S. nigrificans pSN22 replication protein described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid stability protein; replication protein; ethylene forming enzyme; cardrenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase; polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.
                                               GFAAPLRNSG-GLD-VRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPWEI
                                                                    GMDAPLREHGVKLDQVSTWGGDAAK-MATYLAK---GMSQELTGSATKTASKGSYTPFQM
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                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces nigrescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-557827/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shuttle vector.
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                                                                                                                                                                                  VEOE-
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                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-2003
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Length 451;

Score 322; DB 5; Pred. No. 3.2e-23;

16.1%; 30.8%;

Query Match Best Local Similarity

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This sequence is the Brevibacterium lactofermentum pSFK6 protein. The invention relates to a plasmid containing a temperature sensitive invention control region (TSRCR) and a marker gene (MG). The TSRCR is derived from plasmid pAM330 harboured by Brevibacterium lactofermentum (ATCC 13869) and allows the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at an elevated temperature in corpneform bacteria within a temperature range in which the bacteria can grow. The plasmid can be used for modifying a chromosomal gene in a coryneform bacterium, which may be used for the
                              102
                                                                                                                             114
                                                                                                                                                           189
                                                                                                                                                                                                                            --SDAMFDRWISKLVSLGFAAPLR-----NSGGLDVRKIGGEAD-QVLAAYLTKIA 237
                                                                                                                                                                                                                                                                                          281
                                                                                                                                                                                                                                                          175 EPSEAALDEWQGQWRAV-WTAALRKVNPQFTPDDRHGVDFKRLETERDANDLAEYIAKTQ 233
                                                                                                                                                                                                                                                                                                                       234 DGKAPALELARADLKTANGGNVAPFELLGRIGDLTGGMTEDDAAGVGSLEWNLARWHEYE 293
                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is containing a temperature sensitive replication control regions for breeding microorganisms for the production of amino acids by
                                                                                                                                                                                115 GHRAADREGIRDRIGYVGMIRATEVTVGQINGWHPHIHAIVLVGGRTEGERSAKQIVGTF
                              PISGV-----NGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQL
                                                                                                                                                             -----REMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV----SENILESF
                                                                                                                                                                                                                                                                                          ---LELWREFE
                                                            3 PASGVIVAQTAAGTSVVL-----GLMRCGRIWLCPVCAATIRHKRAEEITAAVVEWI
                                                                                                                         55 KRĠGTAYLVTFTARHGHTDRLADLMDALQGTRKTADAPRRPGAYQRLITGGTWAGRRAKD
 Gaps
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temperature sensitive plasmid; TSRCR; protein production; temperature sensitive replication control region; pSFK6.
Indels
                                                                                                                                                                                                                                                                                          SG--VGMEVGSGDGKSGRHGNRAPWEI---AVDAVGG---DPQA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamatsu
                                                                                              103 GTGSVA-MVTMTMRHTAGQRLHDLWTGLSAAWKAATNGRR--
Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                           FGSMGRRAIAWSRGLRARAGLGAELTDA 309

 B. lactofermentum pSFK6 protein sequence.

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 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2000; 2000EP-00105326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum
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 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-573832/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2000.
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15-JAN-2001
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 Matches
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production of useful substances, such as amino acids, by fermentation, to change their genetic traits. Therefore, the plasmid can be used for breading microorganisms for the production of amino acids by fermentation. The plasmid comprises a TSRCR that allows the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. (Updated on 12 -SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                                    80 MGERRIELAIATKNHLAAGGALMMFVGTVRHNRSQSFAQVEAGIKTAYSSMVKTSQWKKE 139
                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                      GMDAPLREHGVKLDQVSTWGGDAAK-MATYLAK---GMSQELTGSATKTASKGSYTPFQM 255
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                                                                                                                                                                                                                                                                                                                      146 REMYGCDGYVRAVEITHG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSL
                                                                                                                                                                                                       ----PISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kanamycin resistant gene; mutation; high temperature resistance;
coryneform microbe; transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brevibacterium lactofermentum p48K protein sequence SEQ ID NO:8.
                                                                                                                                                                            50;
                                                                                                                                               Length 427;
                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 MEBELYKLAGLEAPERVESTRVAVALVKPDDWKLIQS 348
                                                                                                                                              ; Score 318; DB 3; L;
; Pred. No. 7.4e-23;
58; Mismatches 132;
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                                                                                                                                            15.9%;
ilarity 28.8%;
Conservative 58
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                                                                                                                                                                                                      34 LQQITTSETFNACGR--
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(first entry)
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N-PSDB; ABL49734.
                                                                                                                                                           Similarity
                                                                                                                  Sequence 427 AA;
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                                                                                                                                                 Mac
Local Sim-
97;
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29-MAY-2002
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temperature-resistant corputation microbe in which the high temperature-resistant corputation microbe in which the high temperature resistant corpue is treated with a chemical changing the structure of cell wall of the microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall cesistant corpreform microbe in which the cell wall of a high temperature-resistant corpreform microbe is wackened and electric pulse is applied to a solution containing the microbe having weakened cell wall and a DNA; cc (2) a transformant of a high temperature-resistant corpueform microbe in which a recombinant DNA is introduced; and (3) a transformant of a high temperature-resistant corpueform microbe of compinant DNA is introduced; and (3) a transformant of a high temperature-resistant corpueform microbe and a plasmid vector derived from Corpuedacterium glutamicum or Brevibacterium clarcofermentum. The method is used for transforming a high temperature-resistant corpueform microbe. The present sequence represents a lactofermentum lactofermentum p48K protein sequence represents a sample from the present invention. (Updated on 29-AUG-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 MYKITNSKALAGCHRWRRDEAVAVSWSS-----NG--ASQFEGLQNSHSRWGSSLAELEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GAHRADEISQVVAHQLGTGSVAMVTM-TMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMDAPLREHGUKLDQVSTWGGDAAX-MATYLAK---GMSQELTGSATKTASKGSYTPFQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 427;
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MEEELYKLAGLEAPERVESTRVAVALVKPDDWKLIQS 348
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                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 318; DB 5; Le 28.8%; Pred. No. 7.4e-23; ive 58; Mismatches 132;
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Best Local Similarity 28.0.
The 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 427 AA;
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12-FEB-2002
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                                                                                                                                                                                                                                                                                      The present invention relates to Coryneform bacterium in which the arginine repressor does not function normally and which produces Larginine. Coryneform bacterium is used to produce Larginine which is useful in agents for promoting liver function and in amino acid infusions or in 'comprehensive' amino acid pharmaceutical. Coryneform bacterium accumulate Larginine to higher levels than wild-type strains, e.g. 120 compared with 20, mg/dl. The present sequence is Brevibacterium lactofermentum p48K replication control region protein. The replication control region protein and coryneform bacteria and temperature sensitive vector. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 GAHRADEISQVVAHQLGTGSVAMVTM-TMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFAAPLRNSG-GLD-VRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPWEI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 AVDAVGCDPQALE-----LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQI--- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 REMYGCDGYVRAVEITHG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LOQITISETENACGR-----PISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-arginine production, coryneform bacteria; lysE; arginine repressor; argR; liver function promoting agent, amino acid infusion; amino acid pharmaceutical; replication control region; plasmid pSFK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                      Coryneform bacterium with inactivated arginine repressor, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by B. lactofermentum ORF in plasmid pSFK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 318; DB 5; Length 42
28.8%; Pred. No. 7.4e-23;
ive 58; Mismatches 132; Indels
                                                                                                                                                                                                              fermentative production of arginine at high levels
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:| | :|:| | :|:: | :|::| MEEELYKLAGLEAPERVESTRVAVALVKPDDWKLIQS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ESAPVMVAIIPARSWMMIRT 335
                                                                                   Kurahashi
                                                                                   Ä
                                                                                                                                                                                                                                                     Example 1; Page 20-21; 30pp; English.
                                                                                   Ito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB66179 standard; protein; 427 AA
                                                                                 χ,
28-APR-2000; 2000JP-00129167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Corynebacterium glutamicum.
                                                                                   Mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 28.8 97; Conservative
                                     (AJIN ) AJINOMOTO KK
                                                                                 Asakura Y,
                                                                                                                        2002-012660/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEOE---
                                                                                                                                            N-PSDB; AAD22583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003
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Best Local Si
Matches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                                 Suga M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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IID ADB6
XXX AC ADB6
XXX DDT 04-Г
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XX L-aı
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139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microorganism (e.g. coryneform bacteria) that has Larginine producing ability and has been modified for enhanced expression of the lysE gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents the protein encoded by the Erevibacterium lactofermentum ORF in plasmid pSFKG. Note: The present sequence is given as SEQ ID No:7 in the Sequence Listing but is referred to as SEQ ID No:6 in the rest of the specification.
                                                                                                                                                                                                                                                                                                                                                                                      A microorganism comprising enhanced expression of the lysE gene is useful for enhanced production of L-arginine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to a method for producing L-arginine in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 GAHRADEISQVVAHQLGTGSVAMVTM-TMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFAAPLRNSG-GLD-VRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 GMDAPLREHGVKLDQVSTWGGDAAK-MATYLAK---GMSQELTGSATKTASKGSYTPFQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVDAVGGDPQALE-----LWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LQQITTSETFNACGR-----PISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 318; DB 7; Length 427; 28.8%; Pred. No. 7.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|
MEEELYKLAGLEAPERVESTRVAVALVKPDDWKLIQS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 VEQE------ESAPVMVAIIPARSWMMIRT 335
                                                                                                                                                                                                                                                        Yasueda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. lividans pIJ101 replication protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 19-21; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                                                                                                                           Gunji Y,
                                                                                                17-JUL-2002; 2002US-00196232.
                                                                                                                                                     25-JUL-2001; 2001JP-00224586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB84281 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 28.8
Matches 97; Conservative
                                                                                                                                                                                                   (AJIN ) AJINOMOTO CO
                                                                                                                                                                                                                                                        Ito H,
                                                                                                                                                                                                                                                                                                           2003-708853/67.
                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADB66212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 427 AA;
US2003113899-A1.
                                                                                                                                                                                                                                                        Yamaguchi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-2003
                                                19-JUN-2003
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RESULT 13

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145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding replication protein/plasmid stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isoprenoid molecules, polyhydroxyalkanoic hydratases, ethyllene forming enzyme, pyruvate decarboxylase, alcohol dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in Choning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents a Rhodococcus AN12 Rep
                  forming enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                         protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 GHRAADREGIRDKIGYVGMIRATEVTVGQINGWHPHIHAIVLVGGRTEGERSAKQIVATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SDAMFDRWTSKLVSLGFAAPLR------NSGGLDVRKIGGEAD-QVLAAYLTKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG--VGMEVGSGDGKSGRHGNRAPWEI---AVDAVGG---DPQA-----LELWREFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGKAPALELARADLKTATGGNVAPPELLGRIGDLTGGMTEDDAAGVGSLEWNLSRWHEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 KRĠGTAYLVŤFŤARHGHTDRĽAĎĽMDAĽQGTRKTPDSPRRPGAYQRLITGGTWAGRRAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----REMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV----SENILESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
            Plasmid stability protein; replication protein; ethylene forming enz carotenoid biosynthesis enzyme; isopremoid; pyruvate decarboxylase; polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.8%; Score 316; DB 5; Length 456; 30.5%; Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in Rhodococcus sp. This sequence represents a Rhodoco protein described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GTGSVA-MVTMTMRHTAGQRLHDLWTGLSAAWKAATNGRR
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                                                                                                                                                                                                                                                                                                                                     Tomb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGSMGRRAIAWSRGLRARAGLGAELTDA
                                                                                                                                                                                                                                                                                                                                   Kostichka KN,
                                                                                                                                                                                                                                                                                                 В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 4A; 96pp; English.
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                                                                                                                                                                                                                                                              12-DEC-2000; 2000US-0254868P
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                                                                                                                      Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                 Cheng
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-557827/59
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                                                                                    shuttle vector
                                                                                                                                                         WO200255709-A2
                                                                                                                                                                                                                                                                                                                                     Bramucci MG,
                                                                                                                                                                                          18-JUL-2002
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New bacterium of Ketogulonigenium genus, useful for producing 2-keto-L-gulonic acid from sorbose or sorbitol, comprises transgene containing DNA sequence from endogenous Ketogulonigenium plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new bacterium of genus Ketogulonigenium. Ketogulonigenium may further comprise a transgene, comprising a DNA sequence from an endogenous Ketogulonigenium plasmid. Methods for transforming Ketogulonigenium are also described. The invention is useful for producing 2-keto-L-gulonic acid (2-KLG) from L-sorbose or sorbitol. The present sequence represents the replication protein encoded by the Ketogulonigenium endogenous plasmid pADNX6L2. (Updated on 07-AUG-2003 to correct OS field) (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 DGGRRAFFSGLAQCRNVWGCAVCSARIAQIRRSEMNHLLAWARDNGFVPVLITLTAQHKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 L-LMFSGDVSE--NILESFSDAMFDRWTSKLVSLGFAAPLRNSGGLDVRKIGGEADQVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 NGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADBISQVVAHQLGTGSV-AMVTMTMRHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GQRLHDLWTGLSAAWKAATNGRRWRTEREMYGCD----GYVRAVEITHG-KNGWHVHVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 GDSLFDLLQNMKKAKQRLRQRREWR-----DLPFVGSVTSTEITHSYANGWHPHFHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AYLTKIASGVGMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQALELWREFEFGSMG--RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Replication protein encoded by Ketogulonigenium plasmid pADMX6L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 AIAWSRGLRARAGLGAELTD----AQIVEQEESAPVMVAIIPARSWMMIR 334
                                                                                                                                                    Ketogulonigenium, 2-keto-L-gulonic acid, L-sorbose, sorbitol, replication protein, plasmid pADMX6L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 282; DB 5; 30.0%; Pred. No. 3.5e-19;
 466 AA.
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                                                                                                                                                                                                                                                                                                                                                        (ARCH ) ARCHER-DANIELS MIDLAND (DELL/) D'ELIA J. (STOD/) STODDARD S F.
                                                                                                                                                                                                                                                                                                                             05-APR-2000; 2000US-0194627P.
                                                                                                                                                                                                                                                                                              05-APR-2001; 2001WO-US011097
AAU11039 standard; protein;
                                                                                                                                                                                                     Ketogulonicigenium robustum
                                                                                            (first entry)
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                                                               (revised)
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Best Local Similarity
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                                                                                                                                                                                                                                  WO200177348-A2.
                                                           29-AUG-2003
07-AUG-2003
12-MAR-2002
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                                AAU11039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GCDGYVRAVEITEREMY-------GCDGYVRAVEIT 161
                                                                                                                                                                                                                                         Plasmid stability protein; replication protein; ethylene forming enzyme; carofenolab biosynthesis enzyme; isopremoid; pyruvate decarboxylase; polyhydroxyalkamoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding replication protein/plasmid stability protein, useful in cloning and expression vectors, particularly shuttle vectors for expression of heterologous genes in Rhodococcus species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 LQQITTSETFNACGR----PISGVNGVTIVNGPKGSGFG---GLRSCGKGWICPCCAGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNRVSGIDACGGCGRRVLDPDTGV----IYAKSSRGYVVTIGLVRCGRIWFCPECSSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 GAHRADEI-SQVVAHQLGTGSVAMVTMTMRHTAGQRLHD----LWTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 266.5; DB 5; Length 528; 24.8%; Pred. No. 1.5e-17; ive 45; Mismatches 137; Indels 121;
321 QLVWSQGLKEECGL-VELDDDEAMAEVDAARQSGPEIVAEWDNEGWKQVR
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                                                                                                                                                                                                         phaeochromogenes pJV1 replication protein.
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                                                                                                     ABB84282 standard; protein; 528
                                                                                                                                                                                                                                                                                                                                              Streptomyces phaeochromogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-2000; 2000US-0254868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2001; 2001WO-US047868
                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                            shuttle vector.
                                                                                                                                                                                                                                                                                                                                                                                WO200255709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bramucci MG,
                                                                                                                                                                         13-JAN-2003
                                                                                                                                     ABB84282;
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                                                                                     ABB84282
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The inventors claim an inoculum for silage which comprises lactic acid bacteria, esp. Lactobacillus plantarum and E. faecalis, transformed with an exogenous by an enzyme which breaks down an oligosacc-haride and/or a polysaccharide into a fermentable carbohydrate. The exogenous enzyme is especially an alpha-amylase encoded by the DNA sequence in AAM91246, particularly from nucleotides 184 to 2131 (Claims c. sequence in AAM91246, particularly from nucleotides 184 to 2131 (Claims 2, 6 and 10). The transformed lactic acid bacteria can break down polysaccharides in a silage crop to provide a complete source of the fermentable carbohydrates that the lactic acid bacteria conce of the fermentable carbohydrates that the lactic acid bacteria by the transformed lactic acid bacteries which can be used for establishing and maintaining optimal intestinal flora in animals, including chumans. A plasmid contg. the DNA sequence in AAM91248 is claimed. The plasmid is pLH1 or plablo00. (Updated on 03-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                    PKFEPSTDCDTPGCKCKGKGHGVMVSIVRSADDVALIEYLTKNQDGKRERPDSVDQDLEA 296
                                                                                                                                                            Transformed lactic acid bacteria - using exogenous DNA which codes enzyme that breaks down oligosaccharide and/or polysaccharide, used in silage or as a probiotic.
                    237 ASGVGMEVGSGDGKSGR-HGNRAPWEIA-----VDAVGGDPQALE---
                                                                                                                                                                                                            EFGSMGRRAIAWSRGLRARAGLGA---ELTDAQIVEQEESAPV 320
                                                                                                                                                                                                                              Sequence encoded by ORF2 of plasmid pLH1 or pLAB1000.
                                                                     ----VSLGFAAP---LRNSG-GLDVRKIGGEADQVLAAYLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-amylase; lactic acid bacteria; carbohydrate.
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162 HG-KNGWHVHVHALLMFSGDV---
                                                                                                                                                                                                                                                                                                                                AAP93143 standard; protein; 314
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(UYLO-) UNIV CATHOLIQUE LOUVAIN.
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactobacillus plantarum.
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                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
03-OCT-2002
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                                                                                                    237
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                                                                                                                                                                                                                                                                                               RESULT 15
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Sequence 314 AA;

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Ouery Match
Best Local Similarity 22.4%; Pred. No. 0.00017;
Matches 56; Conservative 50; Mismatches 106; Indels 38; Gaps 10;
                                                                                                                                                                    75 KGWICPCCAGKVGAHRADEISQVV--AH-QLGTGSVAMVTMTMRHTAGQRLHDLWTGLSA 131
                                                                         132 AWKAATNGRRWRTEREMYGCDGYVRAVBITHGRUG-WHVHVHALLMFSGDVSENILESFS 190
129 A----ISKLFQYKKPARNLLGYVRSTEITINRNGTYHQHMHVLLFVKFTYFKDSANYIN 183
                                                                                                                                                                                                                           251 SGRHGNRAPWEI-AVDAVGGDPQA-LELWREFEFGSMGRRAIAWSRGL--RARAGLGAEL 306
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279 VDAMLINVDD 288
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80 MGERRIELAIATKNHLAAGGALMMFVGTVRHNRSQSFAQVEAGIKTAYSSMVKTSQWKKE 139
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204
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Best Local Similarity
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30863, A
67, Appl
6, Appli
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Sequence 20, Appl
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                                                                                                                                                                  October 23, 2004, 03:43:51; Search time 26 Seconds (without alignments) 966.712 Million cell updates/sec
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2005
1 MTSVSAEHLSGKDRPPVLVS......HLHYRLPAADVRPPIISVRK 379
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-521-668B-20

US-09-522-991A-17653

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US-09-252-991A-20381

US-09-252-991A-20311

US-09-252-991A-30315

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US-09-568-40-6

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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16.3%; Score 326; DB 3; Length 427; 29.1%; Pred. No. 5.6e-25; tive 58; Mismatches 131; Indels

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	93	ъ.	. 4	414 559	4 4	US-U9-252-991A-222	-22296		Sequence	22296, A	
	92	, Lo	4.6	579	4	US-09-198-452A-918					
	31 92		4.6	612	4	US-09-252-991A	-991A-29283			29283. A	
		92	4.6	671	4	US-09-252-991A-31862	-31862				
		91.5	4.6	430	4	US-09-489-039A	-10370			10370, A	
		s.	4.6	574	4	US-09-489-039A-13400	-13400			13400, A	
		91	4.5	158	4	US-09-252-991A-16612	-16612			16612, A	
		91	4.5	561	4	US-09-252-991A	-16726			16726, A	
		91	4.5	1174	4	US-09-252-991A-29279	-29279			29279, A	
	90	۲.	4.5	611	4	US-09-252-991A	-25119			25119, A	
	89	s.	4.5	415	4	US-09-252-991A	-25764			25764, A	
	8	٦.	4.5	601	4	US-09-252-991A-3058	-30589			30589, A	
		89	4.4	503	4	US-09-252-991A-2352	-23522			23522, A	
		89	4.4	881	4	US-09-252-991A-3170	-31702			31702, A	
		89	4.4	3562	4	US-09-679-279-14	14			14, Appl	
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						ALIGNMENTS					
RESILT	II.T. 1										
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ν,	Sequence 18, Application US/09521668B	8, Ap	plica	tion US	60/	521668B					
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3 	GENERAL INFORMATION	CKMA	TTON								
•	APPLICANT:		NAKAMURA,	A, JUN							
7	APPLICANT:		KANNO, SOHEI	SOHEI							
	APPLICANT:		KIMURA,	EIICHIRO	20						
	APPLICANT:		TSUI,	MATSUI, KAUHIKO	0						
	APPLICANT:		KAMAT	NAKAMATSU, TSUYOSHI	YOSI	II					
	TITLE OF INVENTION:	INVEN	TION:		ERA	RE SENSITIVE	PLASMID F	FOR	CORYNEFORM BACTERIA	RACTERTA	
	FILE REFERENCE: 0010-1093-0	RENCE	0	010	3-0						
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	CURRENT F	TLING	FILING DATE:	2000-03-08	0	-08					
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Sequence 30445, Application US/09252991A

Sequence 304545, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                           Identity of amino acid at the above locations are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 FGGLRS-CGKGWICPCCAGKVGAHRADEISQVV----AHQLG----TGSVAMVTMTMRH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPW 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------REFEFGSMGR-RAIAWSRGLR-ARAG
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                                                                                                                                                                                                                                                                                                                                                       536 IRHAPADGVGGGAGRRAVELGGGGQQNLQRLLVVQVRIAL-HDQGQRAGGVGRGHRGTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGLSAAWKAATNGRRWRTEREMYGCDGYVRA----VEITH------GKNGWHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            712 VDRPHPGVGQRLVGGLEIXRVGRRAEQEAVVL------VGVGDVHLCRVGH---
                                                                                                                                                                                                                                                                                                                          47 GRPISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCA---GKVGAHRADEISQVV----
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                                                                                                                                                                                                                    Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                            --AHQLGTGS-----VAMVTMTMRHTAGQRLHDL-
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                                                                                                                                                                                                                       DB 4;
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21.7%; Pred. No. 0.26;
tive 48; Mismatches 125;
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US-09-252-991A-30345
                                               aeruginosa
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Best Local Similarity 24.54
Matches 104; Conservative
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                       TYPE: PRT
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                      Best Local Similarity Matches 87; Conserv
                                                                                                                        ; LOCATION: (730)
; OTHER INFORMATION:
US-09-252-991A-17653
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US-09-252-991A-30345
                                                                                         NAME/KEY: UNSURE LOCATION: (730)
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Sequence 17653, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                              Sequence 20. Application US/09521668B

Sequence 20. Application US/09521668B

Sequence 20. Application US/09521668B

September 20. Application US/09521668B

September 20. Application:
September 20. Application:
September 20. Application US/09521668B

September 20. Application US/0952166BB

CURRENT APPLICATION UNBER: US/09/521,668B

CURRENT APPLICATION NUMBER: US/09/521,668B

CURRENT APPLICATION NUMBER: US/09/521,668B

SERIOR APPLICATION NUMBER: US/09/521,668B
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Pred. No. 3.7e-24;
58; Mismatches 132; Indels
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312 MEEELYKLAGLEAPERVESTRVAVALVKPDDWKLIQS 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn version 3.0
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Best Local Similarity 28.8%;
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US-09-252-991A-17653
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Qy 335 TCAPTVFGEILGLVEAGATWENLRDHLHYRLPAAD 369	Query Match 4.9%; Score 98.5; DB 4; Length 621; Best Local Similarity 22.4%; Pred. No. 0.31; 11; Gaps 11; Matches 62; Conservative 27; Mismatches 87; Indels 101; Gaps 11; 17 Cy 175 IMFSGDVSENILESFSDAMFDRW	WESULY (WESULY) Sequence 2282, Application US/09252991A Sequence 2282, Application US/09252991A Sequence 2282, Application US/09252991A Sequence 2282, Application US/09252991A Setent No. 6521795 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 1990-02-18 CURRENT APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 LENGITH: 1409 TYPE: PRT CRGANISM: Pseudomonas aeruginosa
	VS-09-252-991A-23181 VS-09-252-991A-23181 Sequence 23181, Application US/09252991A Sequence 23181, Application US/09252991A Sequence 23181, Application US/09252991A Sequence 23181, Application NUCLEIC REPERATION: APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23181 LENGTH: 676 TYPE: RPT COMPANIEN: PRT COMPANIEN: BRT COMPANIENT COMPAN	OY 62 PKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTGSVAMVTMT 113

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360 -TDLIVAIVGVELGLLSNEAYTMYAVVALVIV----TASPALL-IWLEKRA---PPTQEE 410
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--WTGLSAAWKAATNGR 140
                                                                                                                        ----MFSGDVSENILESFS 190
                                                                                                                                                               DAM-FDR--WISKLVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLITKIASGVGMEVGSG 247
                                                                                                                                                                                                                                                                                                           395 MTLPFTRAAWRPLCSAAVLGAALWAAGASAABERRFDLPAQPLAASLSRLAQQAQVQVLFD 454
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; Batent No. 6121029
; Batent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Ligon, James
; APPLICANT: Zirkle, Ross
; APPLICANT: Zirkle, Ross
; APPLICANT: Goerlach, Joern
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GERES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT PILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
                                                          GGGTVALSRRADPPGRSPACRQAGLRYGADRPPRRFSPRPAGAIAGAGAAAGW-
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      --MRHTAGQRLHDL-
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US-09-335-409-11
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## SEQUENCE 30935, Application US/09252991A
## Patent No. 6551795
## GENERAL INFORMATION:
## SEPLICATION
## SEPLICATION
## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## CURRENT PILING DATE: 1099-02-18
## CURRENT FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1998-02-18
## PRIOR FILING DATE: 1998-07-27
## NUMBER OF SEQ ID NOS: 33142
## SEQ ID NO 30935
## LENGTH: 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 LAIAGLRQPGTGVQGDVAAATAQSLAVGQQRRPGRHVEQTALSQAQVAAAAQGNPSAVAV 450
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Best Local Similarity 21.2%; Pred. No. 1.1;
Matches 86; Conservative 50; Mismatches 143; Indels 127; Gaps
                                                                                                                                                                                             14 RPPVLVSSDKRGIRHELR--PKLQQITTSETFNACGRPISGVNGVTI-----VNGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 L-----GT---GSVAMVTMTMRHTAGOR---LHDLWTGLSAAWKAATN-----
                                                                                                                                        Gaps
                                                                                                                               Indels 119;
                                                                       DB 4; Length 1409;
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                                                                                                                                     51; Mismatches 160;
                                                                          4.9%; Score 98.5; 23.8%; Pred. No. 1;
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                                                                          Query Match 4.9%;
Best Local Similarity 23.8%;
Matches 103; Conservative
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US-09-252-991A-30935
             US-09-252-991A-22282
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SEQ ID NO 11
LENGTH: 713
TYPE: PRT
ORGANISM: Sorangium cellulosum
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 713
                                                                                                Query Match
Best Local Similarity
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Matches 78; Conserv
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                                                                                                  APPLICANT: SCHOOL, James
APPLICANT: Molnar, letvan
APPLICANT: Molnar, letvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Goerlach, Joern
TILLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30584
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPREBRUE: 4.30582A
FILE REPREBRUE: 2000-05-10
FRIOR APPLICATION NUMBER: US/09/567,969
CURRENT APPLICATION NUMBER: 09/335,409
FRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
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4.8%; Score 97; DB 3; Length 713;
Best Local Similarity 22.1%; Pred. No. 0.55;
Matches 78; Conservative 38; Mismatches 157; Indels
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                              Sequence 11, Application US/09568102; Patent No. 6346404; GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
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US-09-567-969-11
'Sequence 11, Application US/09567969
'Parent No. 6355457
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            US-09-568-102-11
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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302 MRVDVSQLRTPAAWGTVALLLATATAAKVVPPAALGARLGGLRGSEAALVAVGLNMKGG-- 359
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APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Moinar, Istvan
APPLICANT: Orr Boson
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
ITLE OF INVENTION: WIMBES: US/09/568,480
CURRENT FILING DATE: 10900-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                              411 SARLEREAARRAYIPGVE----RILVPIVAHALPGFATDIVESIVAS---
   Length 713;
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4.8%; Score 97; DB 3; Length 713 ilarity 22.1%; Pred. No. 0.55; Conservative 38; Mismatches 157; Indele
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Patent No. 6355458
GENERAL INFORMATION:
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                                                          201 LVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNR--- 257
                                                                                              ---krkigetvb-itelsvegoapgpsraageasrglarigarikv 496
                                                                                                                                     258 APWEIAVDAVGGDPQALELWREFEFGSMGRRAIAWSRGLRARAGLGAELTDAQIVEQEES 317
                                                                                                                                                                 30 LRPKLQQITTSETFNACGRPISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAH 89
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                                                                                                                                                                                                                  318 APVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDHLHYRLPAADV 370
                                                                                                                                                                                                                                                        ----LEYSFAAADL 586
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APPLICANT: Schupp, Thomas
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Lighon, James
APPLICANT: Zirkle, Ross
APPLICANT: Cyr. Devon
APPLICANT: Gorlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF BPOTHILONES
FILE REPREBACE: 2000-05-10
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
FRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SCHUMARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 713
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4.8%; Score 97; DB 3; Length 713;
Best Local Similarity 22.1%; Pred. No. 0.55;
Matches 78; Conservative 38; Mismatches 157; Indels
411 SARLEREEAARRAYIPGVE----RILVPIVAHALPGFATDIVESIVAS-
                                                                                                                                                                                                                                              552 VLVVVGDPPAAE----RASARRILVPIIG-
                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09568486 Patent No. 6355459
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US-09-568-486-11
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.09-568-486-11
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RESULT 14 US-09-568-472-11 ; Sequence 11, Application US/09568472

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 LVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 APVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDHLHYRLPAADV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Achar, Istvan
APPLICANT: Achar, Istvan
APPLICANT: Achar, Istvan
APPLICANT: Cyr, Devon
APPLICANT: Goellach, Joern
APPLICANT: Goellach, Joern
TILLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-3052A
CURRENT PILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 713
GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Miner, Istvan

APPLICANT: Cyr, Devon

APPLICANT: Cyr, Devon

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4.305924

FILE REFERENCE: 4.305924

CURRENT APPLICATION NUMBER: US/09/568,472

CURRENT FILING DATE: 2000-05-10

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 11

LENGTH: 713
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4.8%; Score 97; DB 3; Length 713;
Best Local Similarity 22.1%; Pred. No. 0.55;
Matches 78; Conservative 38; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/09567899
; Patent No. 6383787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Sorangium cellulosum
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; ORGANISM: Sorangium cellulosum US-09-567-899-11
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Length 713; 57; Indels 80; Gaps	30 LRPKLQQITTSETFNACGRPISGVNGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAH	302 MRVDVSQLRTPAAWGTVALLLATATAAKVVPAALGARLGGLRGSEAALVAVGLNMKGG 359	90 RADEISQVVAHQLGTGSVAMVTMTMRHTAGQRLHDLWTGLSAAWKAATNGR 140	360 -TDLIVAIVGVELGLLSNEAYTMYAVVALVTVTASPALL-IWLEKRAPPIQEE 410	RWRTEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSK 200	: : : HALPGFATDIVESIVAS	201 LVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNR		258 APWEIAVDAVGGDPQALELWREPEFGSMGRRAIAWSRGLRARAGLGAELTDAQIVBQEES	497 GIWRQRRELRGSIQAILRASRDHDLLVIGARSPARARGMSFGRLQDAIVQRAESN	318 APVMVAIIPARSWMMIRTCAPYVFGEILGLVEAGATWENLRDHLHYRLPAADV 370	
ch 4.8%; Score 97; DB 3; Length 713; Similarity 22.1%; Pred. No. 0.55; 78; Conservative 38; Mismatches 157; Indels	CGRPISGVNGVTIVNGPKGS	VALLLATATAAKVVPAALGA	SVAMVIMIMEH	 SNEAYTMYAUVALVTV	AVEITHGKNGWHVHVHALLM	411 SARLERRERARRAYIPGVERILVPIVAHALPGFATDIVESIVAS	DVRKIGGEADQVLAAYLTKI	: -KRKLGETVD-ITELSVEQQ	LELWREFEFGSMGRRALAWSI	: : : : LRASRDHDLLVIGARSPARAI	RTCAPYVFGELLGLVEAGAT	: : RASARRILVPIIG
Similarity 2 8; Conservati	LRPKLQQITTSETFN2	MRVDVSQLRTPAAWGI	RADEISOVVAHOLGTO	-TDLIVAIVGVELGLI	RWRTEREMYGCDGYVE	SARLEREEAARRAYI	LVSLGFAAPLRNSGGI		APWEIAVDAVGGDPOA	: GIWRQRRELRGSIQAI	APVMVAIIPARSWMMI	VLVVVGDPPAAE
Match ocal s 7	30	302	90	360	141	411	201	455	258	497	318	552
Query Match Best Local Matches 7	δλ	qq	ζ	qq	δλ	qa	ολ	qq	ζ	qa	ò	qq

Search completed: October 23, 2004, 03:58:40 Job time: 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 23, 2004, 03:57:47 Run on:

; Search time 85 Seconds (without alignments) 1443.583 Million cell updates/sec

US-10-007-527A-2 2005 1 MISVSAEHLSGKDRPPVLVS......HLHYRLPAADVRPPIISVRK 379 Perfect score:

BLOSUM62 Scoring table:

Sequence:

Gapop 10.0 , Gapext 0.5

1364641 seqs, 323758627 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Published Applications AA:*

1: \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{pubpaa} \) \(\text{VSOT} \) \(\text{FUECOMB.pep:*} \) \(2 \text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{pubpaa} \) \(\text{VSOT} \) \(\text{FW} \) \(\text{PUB.pep:*} \) \(2 \text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FW} \) \(\text{PUB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FW} \) \(\text{PUB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Pubpaa} \) \(\text{VSOT} \) \(\text{FISS PUBCOMB.pep:*} \) \(\text{cgn2} \) \(\text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \(\text{cdata} \) \(2 \text{Fit} \) \('Ggn2_6/ptodated/2/pubpad/USO9B_PUBCOMB.ppp: '
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'Ggn2_6/ptodated/2/pubpad/USO9C_PUBCOMB.ppp: '
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'Ggn2_6/ptodated/2/pubpad/USOOA_PUB.ppp: '

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 2. Appli	Semience 2 Annli	Segmente 2 Appli	Seminary C appear	Segmence 21, April	Semience 21 Appl	Segmence 6. Appli	Sequence 24. Appl	Semence 24 Appl	Semience 24. April	Semience 8 Annli	Segmence 7. Appli	Sequence 22, Appl	
		ΩI.	US-10-007-527A-2	US-10-007-452-2	US-10-415-562A-2	US-10-007-527A-21	US-10-007-452-21	US-10-415-562A-21	US-09-835-381-6	US-10-007-527A-24	US-10-007-452-24	US-10-415-562A-24	US-09-835-381-8	US-10-196-232-7	US-10-007-527A-22	
		DB	14	14	16	14	14	16	σ	14	14	16	σ	14	14	
		Match Length DB							427							
e)e	Query	Match	100.0	100.0	100.0	30.4	30.4	30.4	16.3	16.1	16.1	16.1	15.9	15.9	15.8	
		Score	2005	2005	2005	609.5	609.5	609.5	326	322	322	322	318	318	316	
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.007-452- 415-562A 326-191-9	261	-10-007-452-23 -10-415-562A-2- -10-425-114-65	10-156-761-1079 10-021-660-94 0-437-963-1567	10-437-963-152 10-437-963-156 10-437-963-156	0-3	US-10-378-083-20 US-10-437-963-149861 US-10-437-963-187892	.0-369-49 .0-369-49 .0-014-71	-10-437-963 -10-156-761 -10-014-717	-10-205-032	US-10-437-963-183714 US-10-369-493-15887 US-10-437-963-135632
14 10 14	4 4 4	14 16 15	14 14 16	16	14	15 16 16	14 14 13	16 14 13	14 16	16 14 16
456 456 466	466 466 528	528 528 409	417 647 907	373	532 532	5836 533 515	559 567 713	938 7746 3798	4471 184	321 552 552
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316 316 282 282	282 282 266.5	266.5 266.5 109.5	103.5 103 102	101	99.5	98.5 98 97.5	76 76 76	. 6.	95.5 95	94.5 94.5
14 15 16	18 19 20	21 22 23	24 25 26	23 28 29	30	3 3 3 4 3 3	35 37	3 8 8 9 8 9 9 0	41	4 4 4 6 4 7

ALIGNMENTS

```
APPLICANT: Tond. Jean-Francois
APPLICANT: Brawucci, Michael G.
APPLICANT: Chenap, Qiong
APPLICANT: Chenap, Qiong
APPLICANT: Chenap, Qiong
TILLE OF INVENTION: Rhodococus Cloning and Expression Vectors
FILE REFERENCE: CL1709 US NA
CURRENT APPLICATION NUMBER: US/10/007,527A
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 30
SOFTWARRE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 379
                         Sequence 2, Application US/10007527A; Publication No. US20030044807A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rhodococcus AN12
US-10-007-527A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-007-527A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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ö 9 9 1 MTSVSAEHLSGKDRPPVLVSSDKRGIRHELRPKLQQITTSETFNACGRPISGVNGVTIVN 1 MTSVSAEHLSGKDRPPVLVSSDKRGIRHELRPKLQQITTSETFNACGRPISGVNGVTIVN Gaps .<u>.</u> Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 7.9e-182;

Matches 379; Conservative 0; Mismatches 0; Indels 0;

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121 RIHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNGWHVHVHALLMFSGD 180

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241 GMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQALELWREFEFGSMGRRAIAWSRGLRARA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTSVSAEHLSGKDRPPVIVSSDKRGIRHELRPKLQQITTSETFNACGRPISGVNGVTIVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 379;
                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: E.1. du Pont De Nemours and Company
TITHE OF INVENTION: Rhodococus Cloning and Expression Vectors
TITHE OF INVENTION: Rhodococus Cloning and Expression Vectors
CURRENT APPLICATION NUMBER: US/10/415,562A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 60/254,868
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Bramucci, Michael G.
APPLICANT: Bramucci, Michael G.
APPLICANT: KosticAnd, Kristy N.
TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
FILE REFERENCE: C11709 US NA
CURRENT APPLICATION NUMBER: US/10/007,527A
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
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100.0%; Pred. No. 7.9e-182;
iive 0; Mismatches 0;
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                                                                                                          ; Sequence 2, Application US/10415562A; Publication No. US20040115661A1
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361 LHYRLPAADVRPPIISVRK 379
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ORGANISM: Rhodococcus AN12
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Matches 379; Conservative
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US-10-007-527A-21
                                                                     RESULT 3
US-10-415-562A-2
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APPLICANT: Bramucci, Michael G.
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
APPLICANT: Costichka, Kristy N.
ITTLE OF INVENTION: Rhodococus Cloning and Expression Vectors
FILE REFERENCE: CL1709 US NA
CURRENT APPLICATION NUMBER: US10/10/07,452
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-12-12
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Publication No. US20030093701A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      361 LHYRLPAADVRPPIISVRK 379
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US-10-007-452-2
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US-10-007-452-2
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; Publication No. US20030093701A1
; GENERAL INFORMATION:
    APPLICANT: Tomb, Jean-Francois
    APPLICANT: Cheng, Qiong
    APPLICANT: Cheng, Qiong
    APPLICANT: Cheng, Qiong
    TITLE OF INVENTION: RAddcoccus Cloning and Expression Vectors
    FILE REFERENCE: CL1709 US NA
    CURRENT FILING NUMBER: US/10/007,452
    CURRENT FILING DATE: 2000-11-10-08
    PRIOR APPLICATION NUMBER: 60/254,868
    PRIOR PELING DATE: 2000-12-12
    NUMBER OF SEQ ID NOS: 30
    SOFTWARE: Microsoft Office 97
    SEQ ID NO 21
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                                                                                 DB 14; Length 459;
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                         TYPE: PRT ORGANISM: Arcanobacterium pyogenes
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Matches 148; Conservative
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SEQ ID NO 21
LENGTH: 459
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Publication No. US20040115661A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont De Nemours and Company
TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
TITLE REFERENCE: Cl.7709 US PCT
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR APPLICATION NUMBER: 60/254,868
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                    55 KRGGTAYLVTFTARHGHTDRLADLMDALQGTRKTADAPRRPGAYORLITGGTWAGRRAKD 114
                                                                                                                                                                                                                                                                                                    146 ------REMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV-----SENILESF 189
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                                                                                                                                                                                                                                                                                                                                                                                              3 PASGVIVAQTAAGTSVVL-----GLMRGGRIWLCPVCAATIRHKRAERITAAVVEWI
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                                                                                                                                                                                                                                                                                                                          SG--VGMEVGSGDGKSGRHGNRAPWEI---AVDAVGG---DPQA------LELWREFE
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                                                                                                                                  Gaps
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| Sequence 24, Application No. US20030093701A1
| Publication No. US20030093701A1
| GENERAL INFORMATION:
| APPLICANT: Tomb. Jean-Francois
| APPLICANT: Bramucci, Michael G.
| APPLICANT: Cheng, Qione, Kristy N.
| TITLE OF INVENTION: Rhodoccus Cloning and Expression Vectors
| FILE REFERENCE: CL1709 US NA
| CURRENT APPLICATION NUMBER: US/10/007,452
| CURRENT APPLICATION NUMBER: 60/254,868
| PRIOR APPLICATION NUMBER: 60/254,868
| PRIOR FILING DATE: 2000-12-12
| NUMBER OF SEQ IN OS: 30
| SOFTWANDE: MICHAEL OF SEQ IN OS: 30
| SOFTWANDE: MICHAEL OF SEQ IN OS: 30
| SOFTWANDE: MICHAEL OF SEQ IN OS: 30
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                                                                                                 Length 451;
                                                                                               16.1%; Score 322; DB 14; Length 4: 30.8%; Pred. No. 9.4e-22; ive 41; Mismatches 110; Indels
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Local Similarity 30.8%; Pred. No. 9.4e-22;
les 101; Conservative 41; Mismatches 110:
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            LENGTH: 451
TYPE: PRT
ORGANISM: Streptomyces nigirifaciens
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SEQ ID NO 24
LENGTH: 451
                                                                                                 Query Match
Best Local Similarity 30.9%
Matches 101; Conservative
                                                                 US-10-007-527A-24
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US-10-007-452-24
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SEQ ID NO 24
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| Bublication No. US20030044807A1
| GENERAL INFORMATION:
| APPLICANT Tomb, Jean-Francois
| APPLICANT: Cheng, Qiong
| APPLICANT: Cheng, Qiong
| APPLICANT: Kostichka, Kristy N. TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors
| FILE REFERENCE: CL1709 US NA
| CURRENT APPLICATION NUMBER: US/10/007,527A
| CURRENT APPLICATION NUMBER: 60/254,868
| PRIOR APPLICATION NUMBER: 60/254,868
| PRIOR FILING DATE: 2000-12-12
| NUMBER OF SEQ IN NOS: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 427;
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Pred. No. 3.7e-22;
8; Mismatches 131; Indels
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SOFTWARE: Microsoft Office 97
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Best Local Similarity
Matches 98; Conserv
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US-10-007-527A-24
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---NSGGLDVRKIGGEAD-QVLAAYLTKIA 237
                   49 PISGV-----NGVTIVNGPKGSGFGGLRSCGKGWICPCCAGKVGAHRADEISQVVAHQL 102
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| Publication No. US20040115661A1
| GENERAL INPORMATION:
| APPLICANT: E.1 du Pont De Nemours and Company
| TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
| FILE REPERENCE: CL1709 US PCT
| CURRENT FILING UNTER: US/10/415,562A
| CURRENT FILING DATE: 2003-11-17
| PRIOR FILING DATE: 2000-12-12
| PRIOR FILING DATE: 2000-12-12
| RIOR FILING DATE: 2000-12-12
| SOFTWARE: Microsoft Office 97
| SOFTWARE: Microsoft Office 97
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Best Local Similarity 30.8%; Pred. No. 9.4e-22;
Matches 101; Conservative 41; Mismatches 110; Indels 7
                                                         238 SG--VGMEVGSGDGKSGRHGNRAPWEI---AVDAVGG---DPQA-
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ORGANISM: Streptomyces nigirifaciens
--SDAMFDRWTSKLVSLGFAAPLR
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Patent No. US20020045223A1
GENERAL INFORMATION:
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APPLICANT: ASAKURA, Yoko
APPLICANT: MORI, Yukiko
APPLICANT: ITO, Hisao
APPLICANT: KURAHASHI, Osamu
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US-09-835-381-8
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TITLE OF INVENTION: ARGININE REPRESSOR DEFICIENT STRAIN OF CORYNEFORM BACTERIUM AND TITLE OF INVENTION: FOR PRODUCING L-ARGININE FILE REFERENCE: 206018050 CURRENT APPLICATION NUMBER: US/09/835,381 CURRENT APPLICATION NUMBER: US/09/835,381 PRIOR APPLICATION NUMBER: US/000-129167 PRIOR FILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                      Length 427;
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APPLICANT: GUNJI, YOSHIYA
APPLICANT: YASHODA, HISAAHI
ITILE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
FILE REFERENCE: 225391USO
CURRENT APPLICATION NUMBER: US/10/196,232
CURRENT FILING DATE: 2002-07-17
PRIOR FILING DATE: 2001-07-25
NUMBER: OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                             15.9%; Score 318; DB 9; I 28.8%; Pred. No. 2.1e-21; Live 58; Mismatches 132;
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; Publication No. US20030113899A1
; GENERAL INFORMATION:
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Best Local Similarity 28.8%
Matches 97; Conservative
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Matches 97; Conserv
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LENGTH: 427
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US-10-196-232-7
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US-10-415-562A-22
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SEQ ID NO 22
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                                                146 REMYGCDGYVRAVEITHG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSL 204
                                                                                                   27 MYKITNSKALAGCHRWRRDEAVAVSWSS----NG--ASQFEGLQNSHSRWGSSLAELEV 79
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APPLICANT: Tomb, Jean-Francois
APPLICANT: Cheng, Qiong
Qiong, Qiong
APPLICANT: Cheng, Qiong
Cheng, Qiong
TILLE REFERENCE: CL1709 US NA
FILLE REFERENCE: CL1709 US NA
FILLE REFERENCE: CL1709 US NA
CURRENT APPLICATION NUMBER: US/10/007,527A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR PILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 30-12-12
NUMBER OF SEQ ID NOS: 30-12-12
SEQ ID NO 22
LENGTH: 456
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Best Local Similarity 30.55
Matches 100; Conservative
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| Sequence 22, Application US/10415562A
| Sequence 22, Application US/10415562A
| Publication No. US20040115661A1
| GENERAL INFORMATION:
| APPLICANT: E.I. du Pont De Nemours and Company
| TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
| FILE REFERENCE: CL1709 US PCT
| FILE REFERENCE: CL1709 US PCT
| CURRENT APPLICATION NUMBER: US/10/415,562A
| CURRENT FILING DATE: 2003-11-17
| PRIOR PILICATION NUMBER: 60/254,868
| PRIOR PILING DATE: 2000-12-12
| NUMBER OF SEQ ID NOS: 30
| SOFURARE: Microsoft Office 97
| LENGTH: 456
                                                               APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
FILE REFRENCE: CL1709 US NA
CURRENT APPLICATION NUMBER: US/10/007,452
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR FILING DATE: 2001-12
RUMBER OF SEQ ID NOS: 30
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15.8%; Score 316; DB 14;
Best Local Similarity 30.5%; Pred. No. 3.6e-21;
Matches 100; Conservative 40; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces lividans
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Matches 100; Conservative 40; Mismatches 112; Indels 76; Gaps 15;
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                                                                                                                            55 KRGGTAYLVIFTARHGHIDRLADLMDALQGTRKTPDSPRRPGAYQRLITGGTWAGRRAKD 114
                                                                                                                                                                 146 ------SEMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV----SENILESF 189
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Search completed: October 23, 2004, 04:03:56 Job time: 87 secs

Perfect score:

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Sequence:

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Run on:

Scoring table:

Total number

Searched:

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AB032347 Cloning v
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AJ308231 Corynebac
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M21778 Plasmid plJ
AR475429 Sequence
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AJ133194 Shuttle v
AF092036 Shuttle v
AF092931 Shuttle v
AJ133195 Shuttle v
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D14281 Streptomy
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AY072040 Expressio
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BD106940 Method fo
BD139585 Arginine
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                AY180162 Shuttle VB3788 Actinomyces
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AF092037 Corynebac
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Rhodococcus erythropolis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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B.I. DU PONT DE NÉMOURS AND COMPANY (US)
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AUTHORS
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AXI78757 Rhodococc
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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PheGlyGlulleLeuGlyLeuValGluAlaGlyAlaThrTrpGluAsnLeuArgAspHis 360
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Kostichka,K., Tao,L., Brammucci,M., Tomb,J.-F., Nagarajan,V.
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Submitted (11-NOV-2002) CRED, E.I. Dupont de Nemours
Experimental Station, Wilmington, DE 19880-0128, USA
Location/Qualifiers
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E.I. DU PONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
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Kostichka, K., Tao, L., Brammucci, M., Tomb, J.-F., Nagarajan, V.
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Shuttle vector pRHBR17
artificial sequences; vectors.

(Lases I to 11241)
Rostichka, K., Tao, L., Bramucci, M., Tomb, J.-F., Nagarajan, V., Cheng, Q.
A small cryptic plasmid from Rhodococcus erythropolis:
characterization and utility for gene expression
Appl. Microbiol. Biotechnol. 62 (1), 61-68 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheng, Q.
Direct Submission
Submitted (14-NOV-2002) CR@D, E. I. Dupont de Numours Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuttle vector pRHBR17, complete sequence. AY180162. GI:30313707
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Rhodococcus cloning and expression vectors
Patent: WO 02055709-A 6 18-JUL-2002;
B.I. DU FONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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    /organism="Shuttle vector | /mol_type="unassigned DNA" /db_xref="taxon:214938"

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Shuttle vector pRHBR17
artificial sequences; vectors.
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AXS48647.1 GI:25813615
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Arcanobacterium pyogenes
Arcanobacterium pyogenes
Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Bacteria, Actinomyceteria; Actinomycetaceae; Arcanobacterium.
1 (bases i to 2439)
Billington,S.J., Jost,B.H. and Songer,J.G.
The Arcanobacterium (Actinomyces) pyogenes plasmid pAP1 is a member of the piJ101/pVV1 family of rolling circle replication plasmids
J. Bacteriol. 180 (12), 3233-3236 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APUB3788 2439 bp DNA circular BCT 15-JUN-1998
Actinomyces pyogenes plasmid pAPL, complete plasmid sequence.
U83788
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                                             GlyMetGluValGlySerGlyAspGlyLySerGlyArgHisGlyAsnArgAlaProTrp
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/organism="Arcanobacterium pyogenes"
/organism="Benomic DNA"
/strain="BBR1"
/db xref="taxon:1661"
/plasmid="pAP1"
1. 110
/note="single stranded origin; putative"
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Billington, S.J., Jost, B.H. and Songer, J.G.
Direct Submission
Submitted (06-JAN-1997) Veterinary Science, Unities Lowell Street, Tucson, AZ 85721, USA
Location/Qualifiers
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/function="replication protein"
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/note="site of
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1 linearize pAN12 cloned into the PvuII site of pBR328"

join (9925. 11241,1. .3590)

/organism="Cloning vector pBR328"

/mol_type="genomic DNA"

/db xref="taxon:221946"

359]. .992="genomic DNA"

/mol_type="genomic DNA"
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Conservative:
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/organism="Shuttle vector pF
/mol_type="genomic DNA"
/db_xref="taxon:214938"
/focus
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LABIGTIESVRKCGRVVAPAPLVSLRAKSDGRGAGGAGTUTGSSVWACPVCSAKIAARR
KTDLQQVVDHAVKHGWTVSMLTLTQRHHKGGCLKHLWDALSTAWNRVTSGRRWIEFKE
GPGLVGSVVRANEITHGKHGWHVHSHVLIISEKDPLTSTFVYQRKGGRRRLPYPPEIYM
SSDFIAREWMAGLAKHGWPTDFLBOSGGLDWTVAKDARAIGNYGKWOGTRRLPYPPEIYM
GGFKKARNGRRTPFQILADILSLGDVDDLKLWKEYSKARAIGNYGKWOTSTDALSSEVTL
GGFKKARNGRRTPFQILADILSLGDVDDLKLWKEYSKASFGRRALTWSKGLRDWANLG
VEQSDEEIASEEIGDEAIALFTHDAWRQVRRFGAARLIDVTESGGRAAAYRWIDFREI
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BDGRLVELTSIPPQFVQLIDDAVKSRELLEFEKVNLAVLPRNGGGISTYLTLGEAVHV
PAPVVVEVSE"
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LENGGRNPAQLLTQDQVAGMRKTLGTR"
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GlyLeuArgAlaArgAlaGlyLeuGlyAlaGluLeuThrAspAlaGlnIleValGluGln 314
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                                                                                                                                     ThrPheAsnAlaCysGlyArg---ProlleSerGlyValAsnGlyValThrIleValAsn
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ValSerAlaGluHisLeuSerGlyLysAspArgProProValLeuValSerSerAspLys
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                                                              human
          Farrar, M.D. and Holland, K.T.

Farrar, M.D. and Holland, K.T.

Isolation and characterisation of a cryptic plasmid from the hume skin commensal Propionibacterium granulosum

Unpublished

2 (bases 1 to 3540)

Farrar, M.D. and Holland, K.T.

S Farrar, M.D. and Holland, K.T.

Direct Submitsaion

L Submitted (13-SEP-2002) Skin Research Centre, Division of Microbiology, University of Leeds, Leeds LS2 90T, UK

Location/Qualifiers

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//trans1_table=11
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db_xref="GI:27465057"
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/codon_start=1
/transl_table=11
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product="Tra"
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'gene="rep"
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         1236 TCGTTGAAGCGGGTTGCGTTCTGCGGTCGTGTTGCCGCCTCGGCGGTCGCTTCGGTTGGT 1177
                                                           :::
GTGCGGTGCAGCGACCGGGCCGGTTTCGCTGGGGTTGCAGAGCTGCGGATCGGTCTGG
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||||:::
| CTCGTGTTCCTGGTCGGCGACGCTCTG-----GCGCTGCACCGGTCCATG 772
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                                                                                                 78 IleCysProCysCysAlaGlyLysValGlyAlaHisArgAlaAspGluIleSerGlnVal 97
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                                                                                                                   Val------AlaHisGlnLeuGlyThrGlySerValAlaMetValThrMetThr
                                                                                                                                                                                    1056 GTCGAGACCTGGACTAAGCAC-----GGTGGTCGTGTGGCGTTCATGACGTTCACG
                                                                                                                                                                                                                    114 MetArgHisThrAlaGlyGlnArgLeuHisAspLeuTrpThrGlyLeuSerAlaAlaTrp
                                                                                                                                                                                                                                       :::||||||:::
1005 GTTCGGCACTCTTCAAGGATTCCTTGACGCTGTTTGGGATGGTGTCGCTTCGGGGTGG
                                                                                                                                                                                                                                                                                                   134 LysAlaAlaThrAsnGlyArgArgTrpArgThrGluArgGluMetTyrGlyCysAspGly
                                                                                                                                                                                                                                                                                                                                                                                                     LeuLeuMetPheSerGlyAspValSerGluAsnIleLeuGluSerPheSerAspAlaMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GlyGlyLeuAspValArgLysIleGlyGlyGluAlaAsp---GlnValLeuAlaAlaTyr
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CTGAGGAAGGCCAGTTCCAGGGAAGATCGGCCACGAGTTGACGAACTCCCAGAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 GACGGATGGCGTCGCTGGTGGGGCAGCAGAAGCTCTACGAGTGCTGCGAAGTTGC---
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AJO06662
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RSMFGRWERGYLAAGLGTPLARAQDVQCMSAATGLDHLARYLSKAQFOGKIGHELTNS
QSKTARSALSTRSTWEVLGDAANGLAKEVGLWFEWEKGSRGRRQIGWGAGLRDRLGLM
VEESDDVIAAEEVGSVADTVALITGDGWRRLVGQQKLYECLRSCELGGQAGLARWLQE
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                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-JUN-1998) Dasen G.H., Institute of Food Science,
Laboratory of Food Microbiology, ETH Zurich, LFO G24.2,
Schmelzbergetr, 9, CH-8092 Zurich, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                           putative; rep gene.
Propionibacterium freudenreichii
Propionibacterium freudenreichii
Bropionibacterium freudenreichii
Bacteria; Actinobacteria; Actinobacteridee; Propionibacterineae; Propionibacterium.
                                                                                                                                                                                                                                                                                      Dasen, G.H., Miescher, S., Teuber, M. and Meile, L.
Molecular analysis of plasmid plME108, a plasmid isolated
Propionibacterium freudenreichii
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 2051
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                                          353 ThrTrpGluAsnLeuArgAspHisLeuHisTyrArgLeuPro 366
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127
63
144
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Matches:
Conservative:
Mismatches:
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complement (223. .1434)
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complement(223. .1434)
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Best Local Similarity:
Query Match:
DB:
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1639 CAGTCCCGCATCCTCGACACACCGCGAGAACGGGGCTTCGTGGAACTGGTCACCTGCTGA 1698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 LeuglypheAlaAlaProLeuArgAsnSerGlyGlyLeuAspValArgLysIleGlyGly 223
                                                                  AsnGlyTrpHisValHisValHisAlaLeuLeuMetPheSerGlyAspValSerGluAsn 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete nucleotide sequence and characterization of pSNAl from pinaricin-producing Streptomyces natalensis that replicates by a rolling circle mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replication protein; SpdA protein; SPDB2
                                                                                                                                                                                                                                                                                262 IlealaValAspAlaValGlyGlyAspProGlnAlaLeuGluLeuTrpArgGluPheGlu
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1405 CTCGAATACTTCCGGCAGACCGGTGACAGAGTGGCAGGAGTACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 PheGlySerMetGlyArgArgAlaIleAlaTrpSerArgGlyLeuArgAlaArg---Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1465 AAGGGCACGTTCCGCCGTCGGGCGATCACCTGGAGCCGTGGCCTTCGTGCCGAACTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyLeuGlyAlaGluLeuThrAspAlaGlnIleValGluGluGluGluSerAlaProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 MetValAlaIleIleProAlaArgSerTrpMetMetIleArgThrCysAlaProTyrVal
        ArgGluMetTyrGlyCysAspGlyTyrValArgAlaValGluIleThrHisGly---Lys
                       224 GluAlaAspGlnValLeuAlaAlaTyrLeuThrLysIleAlaSerGly---ValGlyMet
                                                                                                                                                                                                                                                                                                                          GluvalGlySerGlyAspGlyLysSerGlyArgHisGlyAsnArgAlaProTrpGlu---
                                                                                                                                 185 IleLeuGluSerPheSerAspAlaMetPheAspArg---TrpThrSerLysLeuValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendes,M.V.
Direct Submission
Submitted (23-JUN-1999) Mendes M.V., Microbiology, Inbiotec,
REAL 1, Leon, 24006, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces natalensis
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                           1237 GCCGGATTCGAACCGAGCAAGGAACAC----GGCATCACCTGGTCCAAAGTC---
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KORA protein; rep gene; rep
protein; transfer protein.
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883 GCACGAGCGAGGCCAAGCACCTCGCCGACACGCGCACCGCCTGGATGATCACGCTGACG
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                                                                                 Streptomýces lavendulae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                      Submitted (28-DEC-1992) J. Felsberg, Inst. of Microbiology, and Molecular Microbiology Div., Videnska 1083, Prague 4,
                                                                                                                                                            from
                                                                                                               Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                          Felsberg, J., Petricek, M. and Tichy, P. Nucleotide sequence of the mini-plasmid ) Lavendulae-grasserius RIA746 Nucleic Acids Res. 21 (15), 3582 (1993) 93348001
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                                                        natalensis"
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59 ValAsnGlyProLysGlySerGlyPhe---GlyGlyLeuArgSerCysGlyLysGlyTrp

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97

6958 ---ValAla 99 6899 GCCTGGAAGAAGACATCAACGACCGCACGGCGGAGGACTGGGCGGCCATCGAGGAGĠĊĊ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX172684 4603 bp DNA circular BCT 05-SEP-2003 Corynebacterium glutamicum plasmid pAG3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7673 CIGGOGGICATCCIGGCCGACCCIGGCACCAGCACAICGCCCGCCGCAAAGGCCGCTCC 7732
                                                                                                                                                                                                                                                                                           304 AlaGluLeu-----ThrAspAlaGlnIleValGluGlnGluGluSerAlaProVal 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
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                                                                                                                                                                                                                                                                                                                                                                                 284 SerMetGlyArgArgAlaIleAlaTrpSerArgGlyLeuArgAlaArgAlaGlyLeuGly 303
---- valglyMetGluValGlySerGlyAspGly 249
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Submitted (105-NOV-2002) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ProAlaArgSer
                                                                                                                                                                    265 AspalavalGlyGlyAsp---ProGinAlaLeuGluLeuTrpArgGluPheGluPheGly
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Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae;
Bacteria, Actinobacterium
Corynebacterineae; Corynebacterium.
1 (bases 1 to 4603)
Tauch, A., Publer, A., Kalinowski, J. and Thierbach, G.
Plasmids in Corynebacterium glutamicum and their molecular
Classification by comparative genomics
J. Biotechnol. 104 (1-3), 27-40 (2003)
                                                                                                                                LysserGlyArgHisGlyAsnArgAlaProTrpGluIleAla----
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Qy 278 ArgGluPheGluPheGlySerMetGlyArgArgAlaileAlaIrpSerArgGlyLeuArg 297 Db 1029 CTTGAGTGGGAAAAAGGTTCTAAGGGCAGGGGAGTGGTCGGTC		RESULT 13 AE017229 LOCUS AE017229 LOCUS DEFINITION Mycobacterium avium subsp. paratuberculosis str. kl0, section 3 of 16 of the complete genome. ACCESSION AE017229 AE016958 VERSION AE017229 AE017229.1 GI:41395023	S E	JOURNAL Submitted (05-SEP-2003) Biomedical Genomics Center, University of FEATURES Location/Qualifiers Source 1300717 Organism="Mycobacterium avium subsp. paratuberculosis str. kl0" /mol_type="Mycobacterium avium subsp. paratuberculosis /mol_type="Mycobacterium avium subsp. paratuberculosis /mol_type="Mycobacterium" kl0" /mol_type="Mycobacterium" kl	/sub_species="paratuberculosis" /db_xref="taxon:262316" 68	/producT="EchA13" /producT="EchA13" /producT="AA802893.1" /db_xref="G1:4135024" /b_xref="G1:4135024" /kranslation="MGAWTLSEQAGAQPGARPAEELVTYETLDEGRIARIWLNRPDAH NAQSRGLLVQLDEAFYRAEADDAVRVVILAARGKNFSAGHDLGSELALAERQPGPGQH PTFRFROATRDPTAEXTYLGEWHYFFROATRAECHRACKAELLITGDALDALDAGA PTFRFROADNAKFSDVVGVYRMYENFFFRAKKELLITGDALDALDABAYLGM VSKVFPADELADKTLEFARRIAERPTWAALLIKOSVNAASDAMGFTEALRHAFHTHEL GHAHWAAHNENRYPVGLPPDVEDWRNAKFTRLARRDTP" G1031948 /locus tag="WAP0577" /codon stat=1 /codon stat=1	/transT_table=11 /product="Mypothetical protein" /product="Mypothetical protein" /product="Mypothetical protein" /db_xref="GI:41395025" /transLation="MOLSFORTYLITGGGSGIGKGVAAGLVSAGASVMIVGRNPDRL AGAUERIAPLADRAGNGAIRYEPTDVTMEDBOVARAVDATAWHGRLHGAVHCAGGSL TVGPITHTDSRAMRNIYDLNVAGTMYVLKHVGRELVRGGGSFIGISSIAASNTHRWF GPYGYTKSALDHWMIAADELGESWYRVNSIRPGLIRTDLVDASVIGSPEISADYAQC TPLPRVGEVEDVANLAMFLLSDAAGWITGQCINVDGGHMLRRGPDYSSMMVQWFGQDA LRGGV" 19632754 /locus_tag="MAP0578"
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Matches:
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VAVENSAALLGELGRRVREVAPPYDDAALGRDFLTTWFAQLHQQVADIRRRTGARDND
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complement (5262. 6758)
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Bifidobacterium breve
Bifidobacterium breve
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1 (bases 1 to 5750)
0'Riordan,K. and Fitzgerald,G.F.
Molecular characterisation of a 5.75-kb cryptic plasmid from Bifidobacterium breve NCFB 2258 and determination of mode of replication.
FEMS Microbiol. Lett. 174 (2), 285-294 (1999)
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2 (bases 1 to 5750)
O'Riordan, K. and Fitzgerald, G.F.
Direct Submission
Submitted (22-40-1998) Microbiology, Univeristy College Cork,
Western Road, Cork, Ireland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Par protein; putative involvement in plasmid
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SOURCE
ORGANISM
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AUTHORS
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VERSION
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1481 AAGTCGGGCAAGGACGCCGGAACCGCTGCGGCCGAATACATCACAAGATTCAAGGCGAC 1540
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||1064 CAGCGTCTGCCGGGAACTCATGGTGTCCGACAGCTTCGGAAACTACATCTTCGGCACC 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1184 GGCTGGACGAAGATGATTAACGGAAGCCCTTGGCAACGGGCCTTGGAAAATC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 GlyAsnArgAlaProTrpGluIleAlaValAspAlaValGlyGly-----AspProGln 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 AspGlyTyrValArgAlaValGluIleThrHisGlyLysAsnGlyTrpHisValHisVal 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisAlaLeuLeuMetPheSerGlyAspValSerGluAsnIleLeuGluSerPheSerAsp 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 -------AlaAlaProLeuArgAsnSerGlyGlyLeuAspValArg--- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 LysileGlyGlyGluAlaAspGlnValLeuAlaAlaTyrLeuThrLysileAlaSerGly 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 ValGly-------MetGluValGlySerGlyAspGlyLySerGlyArgHis 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 ACCAACGGGGAGAAAGCCCGGTTTACAGGCACCATGCTGTGCGGCTCGATCTGGGCATGC 943
                                                                                                                                                                                                                                                                                   110 ATAACCCCCTCCCTCTCCCGCACCGATTTACGGCGTCTGGCGTATGGTCGCCCGCGCTGAA 769
                                                                                                                                                                                                                                                                                                                                                                             770 AGCCGAAAGATTCTCGTCGTCGTCGCGGTGGCGAAACGCTCGGGATTCGAGCCGATTAAG 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 CIGCCGCGCTGCGCACGCGCCAACCGGTGGAC----ACCGGCGTGGGTGTGTG 883
                                                                                                                                                                                         GTAGCCGCGGAAGCGGCAAGCGGGGGGGGGGCGCCCCTTGGGAAAAGACGAATAAA 709
                                                                                                                                                                                                                                                                                                                                     44
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                                                                                                                                                                                                                                        -----ProValLeuValSerSerAspLysArg-------GlylleArgHisGlu
                                                                                                                                                                                                                                                                                                                                  30 LeuArgProLysLeuGlnGlnIleThrThrSerGluThrPheAsn--
  169
77
15
                                                                                                                                              4 ValSerAlaGluHisLeuSerGly---LysAspArgPro-
Mismatches:
Indels:
Gaps:
                                                                                               US-10-007-527A-2 (1-379) x E17316 (1-2297)
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                                                                                                                          /translation="MTNGEKARPTGTMLCGSIWACPTCSAIIRHERAHEVALAIGNHA EKLRKAAADOWQAEHEGQRLPPELMYSDSFGNYIFGTLLRHDRTMPLAMTLDAILKG WTWINGSPORASERWKIRGFWASIETTYGYMGWHPHIHPWHELDGILDDGGREAMO QWLLDRWKTWKRWAXYKKGONPYNVAPNDEHGIDLQFKSGWAGTAAAEYITKIG GDKGGYTLAQEIARGDIKNGRWGSVNPPQLLDSGCLGLSDFQREDMLEWQATLRRR CITWSRGLKEDMEVELEDEELAEKADELPGLVGVVVPNRVYKDIRKSAPETLADALD AARRENWGVENRYKKDRAKSAPETLADALD AARRENWGSVARLLPGGQVALLPDGGQDAIADGBAKGDYLPTRNSVW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTSGVVVGGIPGSGKTAGMVIVLAIYLSGCCNIHVIDGKGGDDWGWFSEHATTFVRG
DLDTVHDTLLRLDDEMKCRIASMRQRYGSANYWNVQPDKRPPLEVIIIDECQSFFNAK
GILGGKPAKDKAEEITAAATEIVQKGRSGGFLLFAITQKPTTDSLPSALRENCENRIC
FRVKTPRAARAVLGDMPDGSPSPTDIPPARRGGAIIGLATGEDVWCRPAYVSEEEABR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MKWPWNHNTKPEPLPFRLRPFDPATGGITVGKLANGNDATLIVT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3467 TCGATCTGGGCATGCCCCACCTGCTCGCAATCATTGGCCACGAAGGCCCCACGAGGTC 3408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3347 GCAGAACATGAGGGCAGCGTCTGCCGCCGGAACTCATGGTGTCCGACAGCTTCGGAAAC 3288
                                                                                                                                                                                                                                       complement (1926. . 3934)

/note="region conforming to double stranded origin;
nicking site of rolling circle plasmids"

complement (3985. . 4845)
/gene="fisk gene homolog"
/complement (3985. . 4845)
/gene="fisk gene homolog"
/note="hypothetical protein; similar to transfer proteins and Fisk homologs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GlyThrGlySer 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ValAlaMetValThrMetThrMetArgHisThrAlaGlyGlnArgLeuHisAspLeuTrp 126
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/note="Rep; similar to replication proteins of
Streptomyces plasmids and other members of the pC194
family that replicate by a rolling circle mechanism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5750
106
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Matches:
Conservative:
Mismatches:
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                                                                             product="replication protein"
protein_id="AAD34709.1"
db_xref="G1:4972588"
                                                                                                                                                                                                                                                                                                                                                                                                                                     'protein id="AAD34710.1"
'db xref="GI:4972589"
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3287 TACATCTTCGGCACCCTCACCCTGCGCCATGATCGGACAATGCCGCTGGCCATGACCCTT 3228
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3107 TGGCACCCTCACATTCATGTTTCTCGATGGCGATCTGGACGATGGGCAGCGT 3048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCTGCATAACATGGTCGCGTGGCCTCAAGGAAGACATGGAGGTC---GAGGAACTGGAA 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 AspAlaGlnIleValGluGluGluGluSerAlaProValMetValAla---IleIlePro 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 AlaArgSerTrpMetMetlleArgThrCysAlaProTyrValPheGlyGlulleLeuGly 346
                                      ThrGlyLeuSerAlaAlaTrpLysAlaAlaThrAsnGlyArgArgTrpArgThrGluArg
                                                                               GACGCAATCCTCAAGGGCTGGACGAAGATGATTAACGGAAGCCCTTGGCAACGGGCCTCG
                                                                                                                 GluMetTyrGlyCysAspGlyTyrValArgAlaValGluIleThrHisGlyLysAsnGly
                                                                                                                                             GluSerPheSerAspAlaMetPheAspArgTrpThrSer----LysLeuValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                         2987 GCATACAAGAAAAAAGACGGCAACCCCTACAACGTCGCCCC---AACGACGAACACGC
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2870 AAGATTCAAGGCGACAAAGGCGGCGTCACGCTCAGGAAATCGCGCGGGGGGATATC
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Copyright

protein

Run on:

BLOSUM62

Scoring table:

Perfect score:

Sequence:

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Plasmid stability protein; replication protein; ethylene forming en: carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase; polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase; alcohol dehydrogenase; terpene synthase; cholesterol oxidase; gene;
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ABQ81842
AAI99682 0
ABD01551
ABD01556
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AAI99683 0
ABD09766
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ABX34289
                 ABL49733
AAD22582
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AAZ46134
ABQ81845
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ABQ81844
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ACA42440
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ABN59752
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This invention describes a novel nucleic acid encoding a replication protein or a plasmid stability protein. The product of the invention is useful for expression of nucleic acid such as genes encoding enzymes involved in the production of isoprenoid molecules, polyhydroxyalkanoic acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile hydratases, ethylene forming enzyme, pyruvate decarboxylase, alcohol dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents the Rhodococcus ANI2 derived plasmid pANI2 DNA described in the disclosure of the invention
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GlyMetGluValGlySerGlyAspGlyLysSerGlyArgHisGlyAsnArgAlaProTrp
                                                           GluileAlavalAspAlavalGlyGlyAspProGlnAlaLeuGluLeuTrpArgGluPhe
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                                                                                                                   GAAATCGCTGTTGTTGCAGGGGGGGGGATCCACAAGCGTTGGAACTGTGGCGAGAATTT
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 acid (PHA) synthases, carotenoid biosynthesis enzymes, nitrile hydratases, ethylene forming enzyme, pyruvate decarboxylase, alcohol dehydrogenase, terpene synthases, and cholesterol oxidase in an Actinomycetales bacteria. The replication protein or plasmid stability protein are useful in cloning and expression vectors and particularly in shuttle vectors for the expression of homologous and heterologous genes in Rhodococcus sp. This sequence represents the Plasmid pRHBRI71 DNA described in the disclosure of the invention
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nitrile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forming enzyme;
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GluIleAlaValAspAlaValGlyGlyAspProGlnAlaLeuGluLeuTrpArgGluPhe
                  GlyLeuGlyAlaGluLeuThrAspAlaGlnIleValGluGluGluGluSerAlaProVal
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The invention relates to production of aryl carotenoid compounds. The method involves transforming a host cell comprising a cyclic carotenoid having at least one beta-ionone ring with a gene encoding a carotene desaturase (CrtU) followed by growing the transformed host cell. Also provided is a method for regulating aryl carotenoid biosynthesis in a host cell. The method is useful in the production of aryl carotenoids such as isorenieratene and chlorobactene, which are useful in pharmaceuticals, food supplements, animal feed additives, food colorants and cosmetics. The present sequence represents a B. coli-Rhodococcus shuttle plasmid pRHBR17 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                Aryl carotenoid; beta-ionone; carotene desaturase; CrtU; isorenieratene; chlorobactene; pharmaceutical; food supplement; animal feed additive; food colourant; cosmetic; crtO; ds.
                                                                                                                                                                          Production of aryl carotenoids useful in e.g. pharmaceuticals and food colorants involves bioconversion of cyclic carotenoids comprising beta-ionone ring in the presence of carotene desaturase.
                                                                                                                                                             LeuHisTyrArgLeuProAlaAlaAspValArgProProIleIleSerValArgLys 379
                                                            5621 TICGGCGAGATCCTCGGACTCGTCGAAGCTGGCGCGCACTTGGGAAAATCTTCGTGATCAC
                              GETCTTGGGGCAGAACTAAACAGATGCTCGAGATGCTTGAGCAGGAAGAATCTGCCCCGGTC
                                                                                                              PheGlyGluIleLeuGlyLeuValGluAlaGlyAlaThrTrpGluAsnLeuArgAspHis
                GlyLeuGlyAlaGluLeuThrAspAlaGlnIleValGluGluGluGluSerAlaProVal
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1304 CATTICGICATGITICTCGATGGGGATCTGGACGATGGGCGGGGGGAAGGCAA 1363
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                                                                                                                                                                                                      830 CTGCCGCGCTGCGCCTGCGGCCAACCGGTGGAC----ACCGGCGTGGGTCATG 883
                                                                                                                                                                                                                                                                          884 ACCAACGGCGAGAAAGCCCGGTTTACAGGCACCATGCTGTGCGGCTCGATCTGGGCATGC 943
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                                        710 ATAACCCCCTCCCTCTCCCGCACCGATTTACGGCGTCTGGCGTATGGTCGCCGCGCTGAA
                                                                                                                                                                                                                                              60 AsnGlyProLysGlySerGlyPheGlyGlyLeuArgSerCysGlyLysGlyTrplleCys
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----ProvalLeuvalSerSerAspLysArg-
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1838 GACATTGGCAAGAGTGCGCCTGAGACACTGGCCGACGCATTGGATGCCGCCGAACGC--- 1894
                                                                                       332 MetileArgThrCysAlaProTyrValPheGlyGlulleLeuGlyLeuValGluAlaGly 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4; LTI; Streptomyces longisporous; HIV gp120; AIDS; IgG1; T cell; immunoglobulin; surface glycoprotein; virus; MHC class II; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding the chimeric protein V1V2-hCH2-KA.
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/product= "V1V2"
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/product= "CH2"
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P-PSDB; AAR20634.
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immunoglobulin subclass at mediating cell killing by both complement and ADCC. The vectors are used for the prodn. of sol. CD4 chimeric proteins in bacterial hosts, in which the HIV gp120 binding region is joined to a region of the human Ig constant region lacking the CH3 domain, which increases the stability of the CD4, thus increasing the serum half life and/or potency against HIV infection and inhibit virus-induced cell fusion, relative to soluble CD4. See also AAQ20908,9
                                                                                                                                     Revised record issued on 23-SEP-2004 ; Correction to Feature Table Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysGlyLysGlyTrp11eCysProCysCysAlaGlyLysValGlyAlaHisArgAlaAsp
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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This sequence encodes the Brevibacterium lactofermentum p48K protein. The invention relates to a plasmid containing a temperature sensitive replication control region (TSRCR) and a marker gene (MG). The TSRCR is derived from plasmid pAM330 harboured by Brevibacterium lactofermentum (ATCC 13869) and allows the plasmid to replicate autonomously at a low temperature but does not allow the plasmid to replicate autonomously at a low nevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. The plasmid can be used for modifying a chromosomal gene in a coryneform bacterium, which may be used for the production of useful substances, such as amino acids, by fermentation, change their genetic traits. Therefore, the plasmid can be used for
                                                                                                                                              2734
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                                                                                   2794
-ValGlyMetGluValGly 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmids containing a temperature sensitive replication control regions useful for breeding microorganisms for the production of amino acids by
                                                                                                                                                                                              ----LeuGluLeuTrpArgGluPheGluPheGlySerMetGlyArgArgAlalleAla
                           2673 IGGACCCGCIACCIGCGGCAGATGCTCGGGCTCGACGCGGCGACACCGAGGCC 2620
                                                         SerGlyAspGlyLysSerGlyArgHisGlyAsnArgAlaProTrpGluIle----
                                                                                                                                                                                                                                     292 TrpserArgGlyLeuArgAlaArgAlaGlyLeuGlyAlaGluLeuThrAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temperature sensitive plasmid; TSRCR; protein production; temperature sensitive replication control region; p48K; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamatsu T;
                                                                                                                    -AspProGlnAla-.
228 ValLeuAlaAlaTyrLeuThrLysIleAlaSerGly-
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                                                                                                                                                                                                                                                                                                                                                                                                                                    B. lactofermentum p48K coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1318. .2601
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 14-17; 29pp; English.
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                                                                                                                    263 AlaValAspAlaValGlyGly--
                                                                                                                                                                                                                                                                                                                               AAA90934 standard; DNA; 4447 BP.
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1629 TGTGGGCACTGTTCGACACCGCTCACAGTCATTTGCGCAGGTTGAAGCGGGTATTAA 1688
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breeding microorganisms for the production of amino acids by fermentation. The plasmid comprises a TSRCR that allows the plasmid to replicate autonomously at an elevated temperature in coryneform bacteria within a temperature range in which the bacteria can grow. (Updated on 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2153
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                                                                                                                                                                                                                                                                                                              Asn-----GlyvalThrIleval-AsnGlyProLysGlySerGlyPheGlyGlyLeuAr
                                                                                                                                                                                                                                                                                                                                                                      9SerCysGlyLysGlyTrplleCysProCysCysAlaGlyLysValGlyAlaHisArgAl
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                                                                                       U; 0 Other;
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101
58
133
42
                                                                                 Sequence 4447 BP; 824 A; 997 C; 1378 G; 1248 T; 0
                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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2264
                                            2265 GTACAAGCTCGCCGGTCTGGAAGCACCGGAACGGGTCGAATCAACCCGCGTTGCTGTTGC 2324
                               323
          ----ValGluGlnGlu--
                              -GluSerAlaProValMetValAl
                                                                                                                                                          Brevibacterium lactofermentum pSFK6 nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                   Transformation of high temperature-resistant coryneform microbe and
                                                                                                                                                                          Kanamycin resistant gene; mutation; high temperature resistance; coryneform microbe; transformation; gene; ds.
                                                                    allelleProAlaArgSerTrpMetMetileArgThr 335
gAlaGlyLeuGlyAlaGluLeuThrAspAlaGlnIle--
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                              /*tag= a
/product= "pSFK6"
                                                                                                        BP.
                                                                                                      standard; DNA; 4447
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                                                                                                                                                                                                                       1318. .2601
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(first entry)
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                                                                                                                                                                                                Corynebacterium
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The present invention describes a method for transforming a high temperature-resistant coryneform microbe in which the high temperature-centesistant coryneform microbe in which the high temperature-centesistant coryneform microbe is traated with a chemical changing the structure of cell wall of the microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall cresistant coryneform microbe in which the cell wall cand a DNA. Also described are: (1) transforming a high temperature resistant coryneform microbe in which the cell wall and a DNA; (2) a transformant of a high temperature-resistant coryneform microbe having weakened cell wall and a DNA; (2) a transformant of a high temperature-resistant coryneform microbe in convertion microbe in convertion to the high temperature-resistant coryneform microbe and a coryneform microbe and a coryneform microbe and a coryneform coryneform microbe and a coryneform microbe and a coryneform coryneform microbe and a coryneform coryneform microbe and a coryneform microbe and a coryneform microbe carrying both a plasmid vector derived from Coryneform microbe and a coryneform microbe. The present sequence encodes a plasmid vector derived from Coryneform microbe. The present sequence encodes a set of the present invention. (Updated on 29-AUG-2003 to a standardise OS field) Sequence 4447 BP; 824 A; 997 C; 1378 G; 1248 T; 0 U; 0 Other;

Example; Page 16-18; 28pp; Japanese.

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Similarity:
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AGCTGTTGCGGTGTCCTGGTCGTCTAACGGT-----GCTTCGCAGTTTGAGGGTCTGCA 1508
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                                                                                                                                          1396 ATGTACAAGATCACCAATAGTAAGGCTCTGGCGGGGTGCCATAGGTG-GCGCAGGGACGA 1454
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101
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                             Length:
Matches:
Conservative:
Mismatches:
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The present invention relates to Coryneform bacterium in which the arginine repressor does not function normally and which produces Larginine. Coryneform bacterium is used to produce L-arginine which is useful in agents for promoting liver function and namino acid infusions or in 'comprehensive' amino acid pharmaceutical. Coryneform bacterium accumulate L-arginine to higher levels than wild-type strains, e.g. 120 compared with 20, mg/dl. The present sequence is Brevibacterium lactofermentum pSFKK replication control region DNA. This DNA is used in the construction of shuttle vector for Escherichia coli and Coryneform bacteria and temperature sensitive vector. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactofermentum pSFK6 replication control
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                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacteria, arginine repressor; L-arginine; liver function; amino acid infusion; ds.
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                                                                                                                                                                                                                                                                                                                           B. lactofermentum pSFK6 replication control region DNA
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15-SEP-2003

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1629 TGTGGGGACTGTTCGACACCGCTCACAGTCATTTGCGCAGGTTGAAGCGGGTATTAA 1688
1689 GACTGCGTACTCTTCGATGGTGAAAACATCTCAGTGGAAGAAGAAGGTGCACGGTACGG 1748
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                                                                                                                                                                                                                                                      169 lHisValHisAlaLeuLeuMetPheSerGlyAspValSerGluAsnIleLeuGluSerPh 189
                                                                                                                                                                                                                                                                                           eSerAspAlaMetPheAspArgTrpThrSerLysLeuValSerLeuGlyPheAlaAlaPr 209
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                                              1455 AGCTGTTGCGGTGTCCTCGTCTAACGGT-----GCTTCGCAGTTTGAGGGTCTGCA
                                                                gSerCysGlyLysGlyTrplleCysProCysCysAlaGlyLygValGlyAlaHisArgAl
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This sequence encodes the Brevibacterium lactofermentum pSFK6 protein.
The invention relates to a plasmid containing a temperature sensitive
The invention relates to a plasmid containing a temperature sensitive
Carciasely and allows the plasmid to replicate autonomously at a low
temperature but does not allow the plasmid to replicate autonomously at a low
can elevated temperature in coryneform bacteria within a temperature range
in which the bacteria can grow. The plasmid can be used for medifying a
production of useful substances, such as amino acids, by fermentation, to
breeding microorganisms for the production of amino acids by
consideration. The plasmid comprises a TSRCR that allows the plasmid to
replicate autonomously at an elevated temperature in coryneform bacteria
creplicate autonomously at an elevated temperature in coryneform bacteria
within a temperature range in which the bacteria can grow. (Updated on 15
SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is containing a temperature sensitive replication control regions for breeding microorganisms for the production of amino acids by
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                                                                                                                 plasmid; TSRCR; protein production; replication control region; pSFK6; ds.
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 B. lactofermentum pSFK6 coding sequence.

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(revised)
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gSerCysGlyLysGlyTrpIleCysProCysCysAlaGlyLysValGlyAlaHisArgAl

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AAA90951 standard; DNA; 4447 BP

AAA90951

AAA90951 ID AAA9 XX AC AAA9

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1509 AAACTCTCACTCTCGCTGGGGTCATCTCTGGCTGAATTGGAAGTCATGGGCGAACGCCG 1568
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1509 AAACICICACICICGCIGGGGGICAICTICIGGCIGAAIIGGAAGICAIGGGGGAAGGCCG 1568
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91 aAspGluIleSerGlnValValAlaHisGlnLeuGlyThrGlySerValAlaMetValTh 111

71 gSerCysGlyLysGlyTrpIleCysProCysCysAlaGlyLysValGlyAlaHisArgAl

54 Asn-----GlyvalThrlleval-AsnGlyProLysGlySerGlyPheGlyGlyLeuAr

91

53

34 LeuGlnGlnIleThrThrSerGluThrPheAsnAlaCysGlyArgProIleSerGlyVal

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The present invention describes a method for transforming a high temperature-resistant coryneform microbe in which the high temperature-temperature-resistant coryneform microbe in traated with a chemical changing the correction of the containing the microbe and an electric pulse is applied to a solution containing the microbe having a changed structure of cell wall of the microbe in which the cell wall of a high temperature corresistant coryneform microbe is weakened and electric pulse is applied to a solution containing the microbe having weakened cell wall and a DNA; to a solution containing the microbe having weakened cell wall and a DNA; correspond to the microbe having weakened cell wall and a DNA; correspond to the high temperature-resistant coryneform microbe in the high temperature-resistent coryneform microbe and a coryneform microbe and a coryneform microbe and a coryneform microbe and a laceformentum. The method is used for transforming a high temperature-coryneform microbe. The present sequence encodes a laceformentum pass protein sequence, which is used in an example from the present invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transformation of high temperature-resistant coryneform microbe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4447 BP; 827 A; 993 C; 1375 G; 1252 T; 0 U; 0 Other;
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Indels:
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Matches:
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                                                            Location/Qualifiers
1318. .2601
                                                                                                                                                      'product= "p48K"
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30.03%
15.86%
Corynebacterium glutamicum,
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P-PSDB; ABB06342.
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                                                                                                                                                                                                                      JP2002017362-A.
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from

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The present invention relates to Coryneform bacterium in which the arginine repressor does not function normally and which produces L-arginine. Coryneform bacterium is used to produce L-arginine which is useful in agents for promoting liver function and in amino acid infusions or in 'comprehensive' amino acid pharmaceutical. Coryneform bacterium compared with 20, mg/dl. The present sequence is Brevibacterium Lactofermentum p48K replication control region DNA. This DNA is used in the construction of shuttle vector for Escherichia coli and Coryneform bacteria and temperature sensitive vector. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1509 AAACTCTCACTCTGGTGGGGGTCATCTCTGGCTGAATTGGAAGTCATGGGGGAACGCG 1568
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              product= "B. lactofermentum pSFK6 replication control
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                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium with inactivated arginine repressor, useful for fermentative production of arginine at high levels.
                                                                  change
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Conservative:
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proline to serine"
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P-PSDB; AAE13531,
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Best Local Similarity:
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111 rMet---ThrMetArgHisThrAlaGlyGlnArgLeuHisAspLeuTrpThrGlyLeuSe 130
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                                                               yCysAspGlyTyrValArgAlaValGluIleThrHisGly---LysAsnGlyTrpHisVa
                                                                                                                   1749 GGTGGAGCACACCTATAGTGACTATGAGGTCACAGACTCTTGGGCGAACGGTTGGCACTT
                                                                                                                                         169 lHisValHisAlaLeuLeuMetPheSerGlyAspValSerGluAsnIleLeuGluSerPh
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                                               rAlaAlaTrpLysAlaAlaThrAsnGlyArgArgTrpArgThrGluArgGluMetTyrGl
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replace(1255, C)
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/*tag= a
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                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for producing L-arginine in a microorganism (e.g. coryneform bacteria) that has L-arginine producing ability and has been modified for enhanced expression of the lysE gene. The microorganism is also modified so that an arginine repressor (argR) does not function normally. The method of the invention is useful for the enhanced production of L-arginine which is useful in liver function promoting agents, amino acid infusion and comprehensive amino acid pharmaceuticals. The present sequence represents Brevibacterium
                                                                                                                                                                                                                                                  the lysE gene is useful
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Efficient, high-yielding production of ethanol by recombinant coryneform

(REIN-) RES INST INNOVATIVE TECHNOLOGY EARTH.

WPI; 2002-106471/14.

Yukawa H;

2000JP-00181625

16-JUN-2000;

12-JUN-2001; 2001WO-JP004935

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The present invention describes a method for producing ethanol using a coryneform bacterium which is transformed by DNA expressing a pyruvate decarboxylase activity and if required a gene expressing alcohol decarboxylase activity under a regulatory sequence to allow expression under ethanol production conditions. The bacterium does not proliferate under tenanol production conditions. The bacterium does not proliferate transforming the coryneform bacterium which is integrated with a gene expressing a pyruvate decarboxylase activity and if required a gene expressing alcohol dehydrogenase activity under a regulatory sequence coryneform bacterium transformed with the vector of (1). The method is used for producting ethanol. The recombinant bacterium can produce ethanol efficiently with high productivity. The present sequence represents an E. coli/coryneform bacteria shuttle vector having a PDC gene linking with a tac promoter and an ADH gene linking with a tac promoter which is used in
 Im carrying genes expressing pyruvate decarboxylase and optionally
dehydrogenase activity without substantial proliferation.
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Matches:
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6415 TIGGCCGATCAAAGCGACGCCGAGGATATGGACGCTGTTTTGGTGGCTCGGTGGCGT 6356
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Scoring table:

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Sequence 2, Appli
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Sequence 16300, A
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1605 CGGAAAGCCGCCCGGTGCCGCCGGACGCTGTGGCGGATCAGCGGGGACGCCGCG 1546
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Patent No. 6622945
GENERAL INFORMATION:
APPLICANT: TRIPATHI Gyanendra, et al.
TITLE OF INVENTION: 11vidans
FILE REPERENCE: 041144.006
CURRENT APPLICATION UNDER: US/09/754,112A
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH 7560
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ORGANISM: Streptomyces lividans
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Sequence 1, Appli
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                                                                                                      October 23, 2004, 04:02:28 ; Search time 112 Seconds (without alignments) 2405.259 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database :

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Result No.

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42.46%
29.89%
16.81%
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Best Local Similarity:
Query Match:
                                                                                                             Alignment Scores:
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US-09-754-112A-1/C
US-09-754-112A-1/C

Sequence 1, Application US/09754112A

Patent No. 6652945

GENERAL INFORMATION:

APPLICANY: TRIPATHI, Gyanendra, et al.

APPLICANY: TRIPATHI, Gyanendra, et al.

TITLE OF INVENTION: Process for the Production of Polyhydroxyoctanoate by Streptomyce

TITLE OF INVENTION: lividans
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                      ------gĠĊĊTĠATGCGG 1450
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---AsnGlyValThrIleValAsnGlyProLysGlySerGlyPheGlyGlyLeuArgSer
                                          CysGlyLysGlyTrpIleCysProCysCysAlaGlyLysValGlyAlaHisArgAlaAsp
                                                                                         GluileSerGinValValAlaHisGinLeuGlyThrGlySerValAla---MetValThr
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Matches:
Conservative:
Mismatches:
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FILE REFERENCE: 041144.006
CURRENT APPLICATION NUMBER: US/09/754,112A
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 12738
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Cy 228 ValleuhlahafyKleuThrlySileAlaserGlyValGlyMetGluvalGly 245 Db 852 GaCCTGGCGAGTACATCGCAGAGCGCGCCGCCCCCCCCCC	יב אומאומים כי

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138 AsnGlyArgArgTrp---ArgThrGluArgGluMetTyrGlyCysAspGlyTyrValArg 156
                                                                                                                                         Sequence 1, Application US/09371008
Patent No. 6127174
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Masakazu
APPLICANT: SUGIYAMA, Kasakazu
APPLICANT: YOKOZEKI, Kenzo
                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Gluconobacter oxydans
US-09-371-008-1
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40.00%
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10.67%
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Best Local Similarity:
Query Match:
DB:
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US-09-371-008-1/c
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1396 ATGTACAAGATCACCAATAGTAAGGCTCTGGCGGGGGCCATAGGTG-GCGCAGGGACGA 1454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              yCysAspGlyTyrValArgAlaValGluIleThrHisGly---LysAsnGlyTrpHisVa 169
                                                                                                                                                                                                                                                                           91
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                                                                                                                                                                                                                             54 Asn-----GlyValThr1leVal-AsnGlyProLysGlySerGlyPheGlyGlyLeuAr
                                                                                                                                                                                                                                                                          71 gSerCysGlyLysGlyTrplleCysProCysCysAlaGlyLysValGlyAlaHisArgAl
                                                                                                                                                                                                                                                                                                                        91 aAspGluIleSerGlnValValAlaHisGlnLeuGlyThrGlySerValAlaMetValTh
                                                                                                                                                                                                                                                                                                                                        130 rAlaAlaTrpLysAlaAlaThrAsnGlyArgArgTrpArgThrGluArgGluMetTyrGl
                                                                                                                                                                                  LeuGlnGlnIleThrSerGluThrPheAsnAlaCysGlyArgProIleSerGlyVal
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100
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134
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                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Brevibacterium lactofermentum FEATURE: NAME/KEY: CDS
                                                                                1.59e-22
318.00
47.45%
30.03%
15.86%
                                    (1318) .. (2598)
                                                                                                     Percent Similarity:
Best Local Similarity:
                                        ; LOCATION: (131
US-09-521-668B-19
                                                                       Alignment Scores:
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                                                                                                       2324
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------cctctacgggcatctgatgtgtctcgcggttggtgcggtcctcaaa
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3501 CACGATCATGACGTGAGATGTTCGATCCGCGCTTGTGGTTTGCCTGGCAAAGATACTGCC
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2265 GTACAAGCTCGCCGGTCTGGAAGCACCGGAACGGGTCGAATCAACCCGGGTTGCTGTTGC
                                                               -GluSerAlaProValMetValAl
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Plasmid Derived from Gluconobacter Bacteria TITLE OF INVENTION: Plasmid Derived from Gluconobacter Bacteria TITLE OF INVENTION: and a Vector FILE REFERENCE: 0P873 CURRENT APPLICATION NUMBER: US/09/371,008 CURRENT FILING DATE: 1999-08-10 EARLIRE APPLICATION NUMBER: UP 10-227227437 EARLIRE FILING DATE: 1998-08-11 NUMBER OF SEQ ID NOS: 1
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Conservative:
Mismatches:
Indels:
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224443 GGAGACGGTCAACTTGTTGTTGTTGACCGGGACCCCGTA-----CGT

GlyPheGlyGlyLeuArgSerCysGlyLysGlyTrplleCysProCysCysAlaGlyLys

99 224503

224392 CGAGGAGTCCAT----GACCACGGTGGGGAACTTCTCAAGCACGTAGTAGGTGCCATT

105 ---GlySerValAlaMetValThrMetThrMetArgHisThrAlaGlyGlnArgLeuHis 224338 cgggdrcrgdrgccgccgacaccargcccarcgacarggagaggr---crrrrgcac AspLeuTrpThrGly--LeuSerAla---AlaTrpLysAlaAlaThrAsnGlyArgArgT

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224233

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86 ValGlyAlaHisArgAlaAspGluIleSerGlnValValAlaHisGlnLeuGlyThr---

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3063 ATTCACCGGGACGGCGAAAGGCGGCCGTT-----AGTGCGGGCCAGTCGCTCACAGGT 3010
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                                                                               MetPheSerGlyAspValSerGluAsnIleLeuGluSerPheSerAspAlaMetPheAsp 195
                                                                                                                                                                       216 LeuAspValArgLysIleGlyGlyGluAlaAspGlnValLeuAlaAlaTyr---LeuThr 234
                                                                                                                                                                                                                                                                                                                              HisGlyAsnArg-----AlaProTrpGlulleAlaValAspAlaValGlyGlyAspPro 271
                                                                                                                                                                                                                                                                                                            GlnAlaLeuGluLeuTrpArgGluPheGluPheGlySerMetGlyArgArgAlalleAla 291
                                                                                                                                                                                                                                                                                                                                                                   310
                                  157 AlaValGluIleThrHisGly---LysAsnGlyTrpHisValHisValHisAlaLeuLeu
                                                  ArgTrpThrSerLysLeuValSerLeuGlyPheAlaAlaProLeuArgAsnSerGlyGly
                                                                                                                                                  3009 cécnécarcaaccrenideccaagecréchcararcecécrerr---------
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Conservative;
Mismatches:
Indels:
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Fatent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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38.19%
27.99%
6.11%
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US-09-103-840A-1/c
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US-09-103-840A-1
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224114 AGTAG-AACTTG-----CCCGGCAGCGGCAGATGAACGAAATGTGGATGGCGCTTTCG 224062

SerGluAsnIleLeuGluSerPheSerAspAlaMetPheAspArgTrp-------

224173 GGCGGTGTTGGCGGGCC-AGAACTCAAACGGGCGCCAGGGTACCTGAGTCGGGCTCATCC

HisGlyLysAsnGlyTrpHisValHisValHisAlaLeuLeuMetPheSerGlyAspVal

224061 GCCATCGCCCGGTCGGCGATCGGCGAAGTTGATGACGATCGGCTTGGCCACACG 224002

-----ThrSerLySLeuValSerLeuGlyPheAlaAlaPro

198

210

182

224001 ACCATCGCGCCGTCGACCGGATTGAACGTCGGCGGGAACGGCGGCGGCGACAAAC 223942

---LeuArgAsnSerGlyGlyLeuAspVal-----ArgLyslleGlyGlyGluAlaAsp

223882

242 MetGluValGlySerGlyAspGlyLySSerGlyArgHisGlyAsnArgAlaProTrpGlu 261

223881 GGGGGGGGGGGGGGGGGGGGGGGGGCGCCAACGGGTCAAGTGCCGGCGGC---262 IleAlaValAspAlaValGlyGlyAsp-ProGlnAlaLeuGluLeuTrpArgGluPheGl

223941 GATĠTĊGGATCCTGCCCGGCAACGGGCCCCGCTGCTÀĊĊGGCACTĠĊĊĀĠĊĠĠĠTCAĠĠĊ

224115

rpArgThrGluArgGluMetTyrGlyCysAspGlyTyrValArg-AlaValGluIleThr 161

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223738
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                                                          223677 CGGCAACCACTGCGGCTATGTTCAGAGCGGCGGAATAGACTCCCCCTCGTCCAGCCCTGGT
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                                                                                                                                                          -------IleValGluGluGluSerAlaProValMetValAlaIleIl
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                                     281 uPheGlySerMet-----GlyArgArgAlaIleAlaTrpSerArg----
223578 T 223578
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US-09-252-991A-155
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           223824
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CysGlyArgProlleSerGlyValAsnGlyValThrIleValAsnGlyProLysGlySer 65

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 170
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1493 GCCTGA-ATCGCGGGGGGCCGGAAGCGGCCTGGAGTCGGGTGGAGACAGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 aprovalmetvalalallelleproalaargSer------TrpMetMetIleAr
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                                                                                                                                                                                                 248 pGlyLysSerGly-------ArgHisGlyAsnArgAlaProTrpGluIl
              rserlysleuValSerLeuGlyPheAlaAlaProLeuArgAsnSerGlyGlyLeuAspVa
                                                                         218 largLyslleGlyGlyGluAlaAspGlnValLeuAlaAlaTyrLeuThrLyslleAlaSe
                                                                                                     1074 CAGCGCCGAGCCGGCGATCGCCGAGGACGCGGTGCCAGCCTTGCTGGCCGCGGTGCGGA
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1254 CGCGTCGCCGGCATCGCCAGTGCTGCCAGGTGCCAGGCGCATCGAGTT
                                                                                                                                                                                                                                                                                                                         eGlySerMetGlyArgArg---AlalleAlaTrpSerArgGlyLeuArgAlaArgAlaGl
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Mismatches:
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Matches:
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; Patent No. 6551795
                                                                                                                                           238 rGlyValGlyMetGluValGlySer-
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Query Match:
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; ORGANISM: Pseud
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Sequence 155, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 155
FEWARD: 1606
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Mismatches:
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US-09-252-991A-155
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General 175, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
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PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                             313 TITCGTCACCCACCGGGAGAIGCTCGACGATCCGGAACTGGCCGAGCAGGT-GCAACTGC 255
                                                                                                                                                                                                             195 GCGCAACAGGGGCGCTGCACGACGCGCTGCTCGCCG-----AGGGGCGCCGGCCGACCTC 142
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GGTGGACGAGAGATCGTCGGCCTGGTCGAACGCAGCACGGTGAAGGCGATCCGCGAGAT 314
                                                                                                                         --TrpMetMetIleAr 334
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2346 GGGCTTCGCCGCGTCCAGCAGCCGAACCGTTGCCGCTGGCGACGGGCTGTGCTG 2287
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Conservative:
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Best Local Similarity:
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US-09-252-991A-175/c
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US-09-252-991A-175
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1171 CGGCTTCGCCGCCGTGCTCCAGGAGCCGTAGCCGCTGGGCTGTGCTG 1112
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|------GTTCTGCCTGGCCAGCCTGGGGAAGGGCACCAGGCGCTGCTCGAACG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                    113 ThrMetArgHisThrAlaGlyGlnArgLeuHisAspLeuTrpThrGlyLeuSerAlaAla 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpLysAlaAla-----ThrAsnGlyArgTrpArg 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 yLysAsnGlyTrpHisValHis---ValHisAlaLeuLeuMet-------PheSe 178
                                                                                                                                                                                                                                             ValAsnGlyValThrIleValAsnGlyProLysGlySerGlyPheGlyGlyLeuArgSer 72
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                                                                                                                         -----GluLeuArg---Pro
                                                                                                                                                                               LysLeuGlnGlnIleThrThrSerGluThrPheAsnAlaCysGlyArgProlleSerGly
                                                      AlaGluHisLeuSerGlyLysAspArgProProValLeuValSerSerAspLysArgGly
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                     US-10-007-527A-2 (1-379) x US-09-252-991A-170 (1-1803)
Gaps:
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Sequence 2, Application US/09103840A Patent No. 629428 GENERAL INFORMATION. APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.

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Matches:
                   APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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a 1 H 1 1 D	223846 CGGGATCGCCGGAGCCGCGTCCGGGTCCGCCACGCCACG	DB 223726 TCCAGCGCGACATAATTGCTTTCCCTCCGGTGACGTTCT 223688 QY 345 u 345 Db 223687 T 223687 RESULT 11 US-09-22-991A-8370/c Semince R370 Annivation H6/000500013	ield et al. IC ACID AND A INOSA FOR DIA 6 : US/09/252,9 - US-00-18 US-60/074,78	RIOR FILING NOW NOW RECORD FILING TO WISER OF SEQ ID NOS OF DE NOS OF SEQ ID NOS OF SE	: imila I Sir ch: -5277	GGATGC rvalAl GGTTGC CGTGGC

us-10-007-527a-2.rni

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205 lyPheAlaAlaProLeuArgAsnSerGlyGlyLeuAspValArgLysIleGlyGlyGluA 225
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                                                                                                 ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8473
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8473
LENGTH: 3528
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Best Local Similarity:
Query Match:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
APPLICANT: Marc J.
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APPLICANT: Marc J.
APPLICANT: Marc J.
APPLICANT: Marc J.
APPLICANT: Marc J.
APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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877 AAGCCTTAICTGGIGACITIAACGGTIAAGAAI-----GGACCTGAITIACAGGAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                           146 ArgGluMetTyr------GlyCysAspGlyTyrValArgAlaValGluIleThr
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          ; ORGANISM: Nitrosomonas US-09-367-051-2
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US-09-252-991A-8473
                                                       Alignment Scores:
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ArgalabroTrpGlullea ArgalabroTrpGlullea TrpArgGluPheGluPheG ::: TrpArgGluPheGluPheG ::: TrpArgGlyLeuArgASerArgGlyLeuArgA	lakrghladlyLeudlyAla	950 AIGCCGCCCTGGCCGCCGCGCGCGCGCGCGGGTCGTCGTTGGCGCT 1008 409-1 1, Application US/09335409 o. Glillog		IOSYNTHESIS OF EPOTHILONES		Length: 68750 Db Autches: 95 Conservative: 45 Infala: 149	18	ysGlyLysGlyTrpIleCysProCysCysAla 83 Qy :: Db GTGGCCAAGGGTGCCTTCCTCCGCGATGTGCGAG 48295 Db	83		102	122
692 GTGACGACGTGATAGAGCCGTCGGCCTTGCGCACGATG 243 luValGlySerGlyAspGlyLysSerGlyArgHisGlyAsn 243 luValGlySerGlyAspGlyLysSerGlyArgHisGlyAsn 252 GGGTCGGCGAAGATCGCCGCTTCGGGAAACTCGGCGAT. 263 laValAspAlaValGlyGlyAspProGlnAlaLeuGluLeuC 263 laValAspAlaValGlyGlyAspGrGCTGATCCACCAGAAGTCC 283 lySerMetGlyArgArgAlalleAlaTrp	298 laArgAlaGlyLeuGlyAla 890 CGCAGGTCGGTATTGCCGCCGGTG 308 SPAlaGlnIleValGluGlnGluG	RESULT 14 US-09-335-409-1 ; Sequence 1, Application US/09335409 ; Patent No. 6121029	APPLICANT: Schupp, Thomas APPLICANT: Schupp, Thomas APPLICANT: Ligon, James APPLICANT: Molnar, Istvan APPLICANT: Zirkle, Ross APPLICANT: Cyr, Devon	TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF FILE REFERENCE: 4-30582A CURRENT PELLICATION NUMBER: US/09/335,409 CURRENT FILING DATE: 1999-06-17 NUMBER OF SEQ ID NOS: 30	; SCPTWARE: Patentin Ver. 2.0 ; SEQ ID NO 1. i. ENGTH: 68750 ; TYPE: DNA VS-09-335-409-1.	Alignment Scores: 5.13 Score: 117.00 Percent Similarity: 31.25% Best Local Similarity: 5.24%	. Gaps: US-10-007-527A-2 (1-379) x US-09-335-409-1 (1-68750)	65 SerGlyPheGlyGlyLeuArgSerCysGlyLysGlyTrpll	83		92AspGlulleSerGlnValValAlaHis :::	GlyThrGlySerValAlaMetValThrMetThrMetArgHi

YArgArgTrp 142 |||||| ATGACGGTGG 48594 aValGluIle 160 | |-:: CTGCGATTGG 48654 ValAspala 266 |||| |||| GTCAAGGCC 49118 CCTGCTCAG 48535 ArgGlyLeu 296 |||||||| |GCGGCGCG 49295 GlnIleVal 312 :::|||| CATGTGGTG 49355 CGGTCATTC 48713 FICTCGGCC 48773 GGCTCCGT 48833 TrpMetMet 332 ::: GCGGAGCTG 49415 ACGCCGATC 48887 TCTTGGCG 49178 AlaAspVal 370 ||||||| GCGAIGIG 49514 ATTICGIG 49001 |||::: CTGGGCGCG 49061 ACATCCCG 49238 SerGlyAsp 180 ----- 184 SerPheSer 190 AlaProLeu 210 ----- 229 --Glyser 246 ----- 266 ----- 276

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#9515 GCGTTCAGCCTGGCGACGACGCGC 49538
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                                                                                              APPLICANT: Schup, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Likle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Coserlach, Joern
TILE OF INVENTIOR GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT PILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AspGluIleSerGlnValValAlaHis------
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6346404
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity:
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Sequence 1, Application US/10007527A

Publication No. US20030044807A1

GENERAL INFORMATION;

APPLICANT Tomb, Jean-Francois

APPLICANT: Cheng, Qiong

APPLICANT: Cheng, Qiong

APPLICANT: Cheng, Qiong

APPLICANT: Kostichka, Kristy N.

TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors

FILE REFRENCE: CL1709 US NA.

CURRENT APPLICATION NUMBER: US/10/007,527A

CURRENT FILING DATE: 2001-12-05

PRIOR APPLICATION NUMBER: 60/254,868

PRIOR APPLICATION NUMBER: 0200-12-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Microsoft Office 97

LENGTH: 1140
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Perfect score:
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Sequence 2, Appli Sequence 1, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 5, Sequence 7, Sequence 7,

Sequence 7

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Sequence 1, Sequence 5, Sequence 1,

Sequence

Description

Query Match Length DB

Result

Sequence 6, Sequence 6, Sequence 6,

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Sequence 1, Appli Sequence 95384, A Sequence 578, App Sequence 32408, A Sequence 7827, Ap

Sequence 1, Appl. Sequence 96272, A

17 US-10-470-565-1

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Sequence 25453, A Sequence 48219, A Sequence 1, Appli Sequence 1, Appli

7. US-10-437-963-95384 7. US-10-437-963-95384 7. US-10-437-963-32408 7. US-10-815-242-7827 6. US-10-282-122A-30310 6. US-10-282-122A-25453 7. US-10-314-657-1 3. US-10-014-717-1

Sequence 1, Sequence 7, P

Sequence 12, Appl Sequence 6, Appli Sequence 53737, A

US-10-329-079-12 US-10-329-079-6 US-10-437-963-53737

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TYPE: DNA ORGANISM: Rhodococcus AN12

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Mismatches:
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Publication No. US20030093701A1

GENERAL INFORMATION:
APPLICANT: Tomb, Jean-Francois
APPLICANT: Cheng, Olong
APPLICANT: Cheng, Olong
APPLICANT: Cheng, Olong
APPLICANT: Cheng, Olong
FILE REFERENCE: CL1709 US NA
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US/10/007,452
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
LEGGTH 110
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US-10-007-452-1
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Best Local Similarity:
Query Match:
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APPLICANT: Tomb, Jean-Francois
APPLICANT: Bramucci, Michael G.
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors
FILE REFERENCE: CL1709 US NA
CURRENT APPLICATION NUMBER: US/10/007,452
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-12-12
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; Sequence 5, Application US/10007452
; Publication No. US20030093701A1
; GENERAL INFORMATION:
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              Sequence 5, Application US/10007527A
; Sequence 5, Application US/10007527A
; Publication No. US20030044807A1
; GENERAL INFORMATION:
   APPLICANT: Tomb, Jean-Francois
   APPLICANT: Cheng, Qiong
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   PILE REFERENCE: CL1709 US NA
   CURRENT FILING DATE: 2000-12-05
   PRIOR APPLICATION NUMBER: 60/254,868
   PRIOR PILING DATE: 2000-12-05
   PRIOR FILING DATE: 2000-12-12
   NUMBER OF FILING DATE: 2000-12-12
   NUMBER OF SEQ ID NOS: 30
   SOFTWARE: Microsoft Office 97
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US-10-007-527A-5/c
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LENGTH: 6334
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US-10-007-527A-5
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Db 2091 ATGGTGCGATCATTCCGGCGCGATCGTGGATGATTCGGACTTGTGCGCCTTACGTC 2032 Qy 341 PheGlyGlu1leLeuGlyLeuValGluAlaGlyAlaThrTrpGluAsnLeuArgAspHis 360	Qy 361 LeuHisTyrargLeuProAlaAlaAspValArgProProIleIleSerValArgLys 379	RESULT 6 US-10-415-562A-5/c i Sequence 5, Application US/10415562A i Publication No. US20040115661A1 i GENERAL INFORMATION: APPLICANT: E.I. du Pont De Nemours and Company i TILE OF INVENTION: Rhodococcus Cloning and Expression Vectors	CURRENT APPLICATION NUMBER: US/10/415,562A CURRENT FILING DATE: 2003-11-17 PRIOR APPLICATION NUMBER: 60/254,868 PRIOR FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 30 SOFTWARRE: Microsoft Office 97 SOFTWARRE: Microsoft Office 97	; LENGTH: 6334 ; TYPE: DNA ; ORGANISM: Rhodococcus AN12 US-10-415-562A-5	Alignment Scores: 7.46e-215 Length: 6334 Score: 2005.00 Matches: 379 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 DB: 170.00\$ Gaps: 0	-10-007	DB 3051 ATGACCAGCGTAAGTGCTGAACACCTTTCCGGCAAAGACCGGCCTCCCGTGTCG 2992 QY 21 SerAsplySargGlylleargHisGluLeuargProLysLeuGlnGlnIleThrThrSer 40	2991 41 2931 61	Db 2871 GGTCCGAAAGGTTCTGGTTTTCGTTCCTCCTCCTCCGGAAGGGTTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2811	DD 2751 CAACTCGGGACTGGATCTGTTGCGATGGTGACGATGCCATGCGCCATACAGCTGGTCAG 2692 QY 121 ArgLeuHisAspLeuTrpThrGlyLeuSerAlaAlaTrpLysAlaAlaThAsnGlyArg 140	160	
Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 14 Gaps: 0 US-10-007-527A-2 (1-379) x US-10-007-452-5 (1-6334)	Qy 1 MetThrSerValSerAlaGluHisLeuSerGlyLysAspargProProValLeuValSer 20	Qy 21 SerAspLysArgGlylleArgHisGluLeuArgProLysLeuGlnGlnIleThrThrSer 40 Db 1	BPro	Qy 101 GlnLeuGlyThrGlySerValAlaMetValThrMetThrMetArgHisThrAlaGlyGln 120	QY 121 ArgLeuHisAspleuTrpThrGlyLeuSerAlaAlaTrpLysAlaAlaThrAsnGlyArg 140 Db 2691 CGGCTCCACGACCTATGGACTGGACTTTCGGCAGCCTGGAAAGCTGCGACGACGGTCGT 2632 QY 141 ArgTrpArgThrGluArgGluMetTyrGlyCysAspGlyTyrValArgAlaValGluIle 160 Db 2631 CGTTGGCGTACGGAAATGTACGGCTGCGACGACGCCTGTTCAAATC 2572	161 ThrHisGlyLysAsnGlyTrpHisValHisValHisAlaLeuLeuMetPheSerGlyAsp 	181 2511	Oy 201 LeuValSerLeuGlyPheAlaAlaProLeuArgAsnSerGlyGlyLeuAspvalArgLys 220		261	Ala GCT	21	

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Sequence 7, Application US/10007527A

Sequence 7, Application US/10007527A

Publication No. US20030044807A1

GENERAL INFORMATION:

APPLICANT: Tomb, Jean-Francois

APPLICANT: Cheng, Qiong,

APPLICANT: Cheng, Qiong,

APPLICANT: Cheng, Qiong,

APPLICANT: Cheng, Visity N.

TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors

TILE REFERENCE: CL1709 US NA

CURRENT APPLICATION NUMBER: US/10/007,527A

CURRENT FILING DATE: 2001-12-05

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 7

LENGTH: 9652
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ORGANISM: Plasmid
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Pred. No.:
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| Publication No. US20040115661A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: E. INFORMATION:
| TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors
| TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors
| TITLE REFERENCE: CL1709 US PCT |
| CURRENT PAPLICATION NUMBER: US/10/415,562A |
| PRIOR APPLICATION NUMBER: 60/254,868 |
| PRIOR APPLICATION NUMBER: 60/254,868 |
| PRIOR APPLICATION NUMBER: 60/254,868 |
| PRIOR PRING PAIR: 2000-12-12 |
| SEQ ID NOS: 30 |
| SOFTWARE: Microsoft Office 97 |
| LENGTH: 9652 |
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                                                                                                  Sequence 7. Application US/10007452;
Publication No. US20030093701A1;
GENERAL INFORMATION:
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Cheng, Qiong
APPLICANT: Cheng, Qiong
APPLICANT: Kostichka, Kristy N.
TILE OF INVENTION: Rhodococus Cloning and Expression Vectors
FILE REFERENCE: C11709 US NA
CURRENT APPLICATION NUMBER: US/10/007,452
CURRENT FILING DATE: 2001-11-08
PRIOR PRILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
LENGTH: 9652
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COGANISM: Plasmid pRHBR17
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                                          Sequence 6, Application US/10007527A

Publication No. US20030044807A1

FUBLICARIT Tomb, US20030044807A1

APPLICANT Tomb, Jean-Francois

APPLICANT Bramucch, Michael G.

APPLICANT Cheng, Qiong

APPLICANT Cheng, Qiong

APPLICANT Cheng, Qiong

TITLE OF INVENTION: Rhodococus Cloning and Expression Vectors

FILE REFERENCE: CL1709 US NA

CURRENT FILING DATE: 2001-12-05

PRIOR PRILICATION NUMBER: 60/254,868

PRIOR PRILICATION NUMBER: 60/254,868

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ IO NOS: 30

SOFTWARE: Microsoft Office 97
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Publication No. US20030093701A1
GENERAL INPORMATION:
APPLICANT: Tomb. Jean-Francois
APPLICANT: Cheng. Qiong
APPLICANT: Cheng. Qiong
APPLICANT: Cheng. Qiong
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APPLICANT: Cheng. Clong
TITLE OF INVENTION: Rhodococcus Cloning and Exp)
TITLE OF INVENTION: Rhodococcus Cloning and Exp)
TITLE OF INVENTION: Rhodococcus
CURRENT PRILING DATE: 2001-11-08
PRIOR PRILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/254,868
PRIOR PRILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 30
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                                                                                                                                                                                                                      GlyLeuGlyAlaGluLeuThrAspAlaGlnIleValGluGlnGluGluSerAlaProVal
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                        GlyMetGluValGlySerGlyAspGlyLySSerGlyArgHisGlyAsnArgAlaProTrp
                                                                                      GluIleAlaValAspAlaValGlyGlyAspProGlnAlaLeuGluLeuTrpArgGluPhe
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Mismatches:
                     RESULT 12
US-10-415-52A-6/C
; Sequence 6, Application US/10415562A
; Publication No. US20040115661A1
GENERAL INFORMATION:
; APPLICANT: B.I. du Pont De Nemours and Company
; TILE OF INVENTION: Rhodococcus Cloning and Expres;
; CURRENT APPLICATION NUMBER: US/10/415,562A
; CURRENT FILING DATE: 2003-11-17
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                               Indels:
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CRGANISM: Plasmid pRHBR17
US-10-415-562A-6
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                                                                 TYPE: DNA ORGANISM: Streptomyces lividans
      NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 12738
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Publication No. US20020090687A1
GENERAL INFORMATION:
APPLICANT: TRIPATHI, Gyanendra, et al.
TITLE OF INVENTION: Process for the Production of Polyhydroxyoctanoate by Streptomyce TITLE OF INVENTION: 11vidans
FILE REPERBNCE: 041144.006
CURRENT APPLICATION NUMBER: US/09/754,112A
CURRENT FILING DATE: 2001-01-05
                                             -GGCCTGATGCGG 1450
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                            CysGlyLysGlyTrpIleCysProCysCysAlaGlyLysValGlyAlaHisArgAlaAsp
                                                                                     GlulleSerGlnValValAlaHisGlnLeuGlyThrGlySerValAla---MetValThr
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Sequence 5, Application US/09835381

GENERAL INFORMATION:
APPLICANT: SUGA, Mikiko
APPLICANT: TOV, Hisao
APPLICANT: TOV, Hisao
APPLICANT: TOV, Hisao
TITLE OF INVENTION: FOR PRODUCING L-ARGININE
FILE REFERENCE: 206018030
FILE REFERENCE: 206018080
CURRENT APPLICATION NUMBER: US/09/835,381
CURRENT PILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US/09/835,381
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
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Matches:
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US-09-835-381-5
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 23, 2004, 03:42:56 ; Search time 24 Seconds (without alignments) 1519.423 Million cell updates/sec Run on:

Perfect score:

US-10-007-527A-2 2005 1 MTSVSAEHLSGKDRPPVLVS......HLHYRLPAADVRPPIISVRK 379 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 3 2 ::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	, I.,	cnetical ;	•	hypothetical prote		124	replication protei	replication profei	rena protein - Sty	Cation	בייים לינים לינים אולים לינים	prasmin teplicatio	probable traces	propante cype II s	replication initia		ם ם	rep protein - Baci		iolD protein [impo		probable hemadalut	genetic exchange n	probable acv1-Coa	nolykatida symthas	rifomedia politica	probable realizati	Tolactate debuteden	Jactate denydrog	changania denyarog	hypothetical prote
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rep protein - Streptomyces lividans plasmid pIJ101 C;Species: Streptomyces lividans C;Species: Streptomyces lividans C;Date: 28 Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004 C;Accession: A31844 R;Kendall, K.J.; Cohen, S.N. J. Bacteriol. 170, 4634-4651, 1988 A;Title: Complete nucleotide sequence of the Streptomyces lividans plasmid pIJ101 and c

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31	3 8	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

\$34850 hypothetical protein - Streptomyces lavendulae plasmid pSLG33 C;Species: Streptomyces lavendulae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999	R;Felsberg, J.; Petricek, M.; Tichy, P. Nucleic Acids Res. 21, 3582, 1993 A;Tiele: Nucleotide sequence of the mini-plasmid pSLG33 from Streptomyces lavendulae-g-A;Reference number: S34850; MUID:93348001; PMID:8346038	A; Scalus: preliminary; translation not shown A; Scalus: preliminary; translation not shown A; Modecule type: DNA A; Residues: 1-256 < FEL> A; Cross-references: EMBL:X69872 C; Genetics: A; Genome: plasmid pSLG33	Query Match 16.0%; Score 321.5; DB 2; Length 256; Best Local Similarity 33.2%; Pred. No. 8e-19; Matches 85; Conservative 45; Mismatches 105; Indels 21; Gaps 11;		1 MVILTARHKKHHELEPLFDAVANGWRKILSGRAWAGDPKRGVLGERDRLGVRG 161 THG-KNGWHVHVHALLMFSGDVSENILESFSDAMFDR-WTSKLVSLGFAAPLR	61	VY 219 RKIGGRADQVLAAYLTKIASG-VGMEVGSGDGKSGRHGNRAPWE-IAVDAVGGDPQALEL 276	QY 277 WREPERGSMGRRALAWSRGLRAR-AGLGAELTDAQIVEQEESAPVMVALIPARSWMMIRT 335
	.avendulae-g:		11;	160	60 218	116	276 174	335 233

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hypothetical protein 1 - Corynebacterium glutamicum c; Species: Corynebacterium glutamicum c; Species: Corynebacterium glutamicum c; Species: Corynebacterium glutamicum C; Species: 12-Aug-1996 #text_change 09-Jul-2004 C; Date: 12-Aug-1996 #text_change 09-Jul-2004 C; Caccession: 140335 M; Mawa, K.; Teuchiya, M.; Takagi, H.; Morinaga, Y.; Nakamori R; Yamaguchi, R.; Terabe, M.; Miwa, K.; Teuchiya, M.; Takagi, H.; Morinaga, Y.; Nakamori Agric. Biol. Chem. 50, 2771-2778, 1986 A; Tercession: 140335 A; Tercession: 140335 A; Reference number: 140335 A; A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA
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C;Superfamily: replication protein
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                                                                                                                                                                                                                                                                                   299 AEYETAVSGAGHRVDPLPAPAPGPDRRRHRGRRHGRPVPDRRRRFRDGVQIWDRAWNGL 358
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C;Bpecies: Lactobacillus hilgardii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: B35390
B;Doson, K.; Sobcaert, P.; Michiels, F.; Joos, H.; Mahillon, J.
J. Bacteriol. 172, 3089-3099, 1990
A;Title: Lactobacillus hilgardii plasmid plaB1000 consists of two functional A;Accession: B35390; MUD:90264300; PMID:2188951
A;Accession: B35390
A;Steutus: prediminary
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                                                                                                                                                                                                                                                                                                                                               303 GAELTDAQIVEQEESAPVMVAII-----PARSWMMIRTCAPY----VFGEILG 346
                                                                                                                                                                                                                                                                                                                                                                                359 VGRSLDLAVVEAVEGREISMDALGELVQSAGQSRAFLRVLTPQEVTELYDELIG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAELTDAQI----VEQE------ESAPVMVAIIPARSWMMIRT 335
DRWISKLVSLGFAAPLRNSGGL----DVRKIGGEADQVLAAYLTKIASGVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 127; DB 2; Length 314, 22.0%; Pred. No. 0.0081; artive 50; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
                                                                                                                    ---RAPWEIAVDAVGGDPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.4%; Score 169; DB 2;
Best Local Similarity 32.0%; Pred. No. 2.2e-06;
Matches 54; Conservative 28; Mismatches 53
                                                                                                                          -----MEVGSGDGKSGRHGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                               REFEFGSMG--
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A; Residues: 1-314 <JOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-437 <BOD.
A,Cross-references: UNIPROT:052205; EMBL:X03756
A,Note: the authors translated the codon TGG for residue 59 as Arg, CGG for residue 187
A,Note: the authors translated the streptomyces cyanogenus
A,Note: the source is designated as Streptomyces cyanogenus
A,Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SAAWKAATNGRRWRTEREMY 149
                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                 49 PISGV-----NGVIIVNGPKGSGFGGLRSCCKGWICPCCAGKVGAHRADEISQVVAHQL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGSVA-MVTMTMRHTAGQRLHDLWTGLSAAWKAATNGRR-----WRTB---- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 KRĠGTAYLVTFTARHGHTDRLADLMDALQGTRKTPDSPRRPGAYQRLITGGTWAGRRAKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SDAMFDRWISKLVSLGFAAPLR-----NSGGLDVRKIGGEAD-QVLAAYLIKIA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG--VGMEVGSGDGKSGRHGNRAPWEI---AVDAVGG---DPQA-----LELWREFE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces sp. plasmid pSB24.2
C;Species: Streptomyces sp.
C;Date: 07-un-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Date: 07-un-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04020
R;Bolotin, A.P.; Sorokin, A.V.; Aleksandrov, N.N.; Danilenko, V.N.; Kozlov,
Dokl. Biochem. 283, 260-263, 1985
A;Title: Nucleotide sequence of DNA of the actinomycete plasmid pSB24.2.
A;Reference number: S04020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 GVTIVNGPKGSGFG-GLRSCGKGWICPCCAGKVGAHRADEISQVVAHQLGTGSVA-MVTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TARHTAADRLSDLMDALQGTRADAETGTKRRPGAYQRLITGAAW--AGDKRKKSNQEGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----REMYGCDGYVRAVEITHGK-NGWHVHVHALLMFSGDV----SENILESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        3. PASGVIVAQTAAGTSVVL-----GLMRCGRIWLCPVCAATIRHKRAEEITAAVVEWI
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 437;
                                                                                                                                                                                                                                                           Length 456;
                                                                                                                                                                                                                                                                                                                 Indels
              A;Reference number: A91888; MUID:89008081; PMID:3170481
A;Accession: A31844
A;Molecule type: DNA
A;Residues: 1-456 <KEN>
C;Genetics: NNIPROT:P22406
A;Genetics: A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.5%; Score 230.5; DB 2; 24.6%; Pred. No. 4.1e-11; iive 43; Mismatches 140;
                                                                                                                                                                                                                                                                                                                    40; Mismatches 112;
                                                                                                                                                                                                                                                        Score 316; DB 2;
Pred. No. 4.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGSMGRRAIAWSRGLRARAGLGAELTDA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ||||| |:| || || || 294 RATRGRRAIEWTRYLRQMLGLDGGDTEA
                                                                                                                                                                                                                                                                 15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TMRHTAGORLHDLWTGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 24.6
Matches 102; Conservative
                                                                                                                                                                                                                                                                 Query Match 15.84
Best Local Similarity 30.55
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
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Best Local S
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S04020
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Cipe process: Streptococcus thermophilus (strain No.29) plasmin psrl
Cipate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cipate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cipate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cipate: 03-May-1995
Riffashiba, H., Takiguchi, R.; Joho, K.; Aoyama, K.; Hirota, T.
Biosci. Biotechnol. Biochem. 57, 1646-1649, 1993
A;Title: Identification of the replication region of Streptococcus thermophilus No.29 I
A;Reference number: JN0856; MUID:94080026; PMID:7764262
A;Recession: JN0856
A;Accession: JN0856
A;Accession: JN0856
A;Residues: 1-315 - HAAS
A;Cross-references: UNIPROT:Q9RNV8; UNIPROT:Q9RNW4
A;Residues: L-315 - HAAS
A;Cross-references: UNIPROT:Q9RNV8; UNIPROT:Q9RNW4
C;Genetics:
A;Genome: plasmid
C;Superfamily: replication protein
C;Keywords: replication initiation
                                                                                                                                                                                                                                                                                                                                                                                                                           58 IVNGPKGSGFGGLR----SCGKGWICPCCAGKVG---AHRADEISQVVAHQLGTGSVAM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GNLKLYQAYFC-KNKLCPMCNWRRSMKYSYQTRSIVDEAIKQSPKGRFLF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 VTMTMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNG--W 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISETFNACGRPISGVNGVT 57
                                                                                                                                                                                                                   12 KORPPVLVSSDKRGIRHELR-PKLQQITTSETFNACGRPISGVNGVTIVNGPKGSGFGGL
                                                                                                                                                                                                                                                                                                                                                   52 -SCGDTLQFIQNQDGTLKLYQAYFCKNKLCPMCNWRRSMKYSYQTSRIVDBAIKQSPKGR
                                                                                                                                                                                                                                                                                                                                                                                             107 VAMVIMIMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNG
                                                                                                                                                                                                                                                                                                                --KGWICPCCAGKVGAHRADEISQVV---AHQLGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication protein A - Synechocystis sp. plasmid pCA2.4
C;Species: Synechocystis sp.
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A40651
R;Yang, X.; McFadden, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KKQGEILVDKNSRGKERDWRGRKILSLKLADIFKELQYKKTFVERVISCGDTLQFIQNQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reps protein - Streptococcus thermophilus (strain No.29) plasmid pST1
                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                         Length 315;
                                                                                                                                                                                                                                               | : :|| : || : | | : | | : | KKQGEILVDKNSRGKERDWRGRKILSLKLADIFKELQYKKTFVERVI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 315;
                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --WHVHVHALLMFSGDVSENILESFSDAM----FDRWTSKL
                                                                                                                               6.1%; Score 122.5; DB 2;
21.6%; Pred. No. 0.019;
tive 40; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 118.5; DF
22.4%; Pred. No. 0.04;
tive 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KDRPPVLVSSDKRGIRHELRP----KLQQI-
                                     A,Gene: repA
A,Genome: plasmid pER35
C,Superfamily: replication protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                           48; Conservative
                                                                                                                                                    Local Similarity
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nes 52; Conserv
                                                                                                                                                                                                                                                                                                           71 RSCG----
                                                                                                                           Query Match
Best Local S:
Matches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptococcus thermophilus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S2571
EMS Microbiol. Lett. 95, 175-180, 1992
A;Title: Sequencing and characterization of pST1, a cryptic plasmid from Streptococcus t A;Reference number: S25721
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss.references: UNIPROT:Q56129; EMBL:X65856; NID:g47880; PIDN:CAA46686.1; PID:g47881
C;Superfamily: replication protein
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144800
C;Species: Streptococcus thermophilus plasmid pER35
C;Species: Streptococcus thermophilus
C;Species: Streptococcus thermophilus
C;Dates: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Dates: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
R;Solow, B.T.; Somkuti, G.A.
Submitted to the EMBL Data Library, August 1999
A;Description: Comparison of low molecular weight heat stress proteins encoded on plasmi
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KSRLCPLCNWRRSMGQSNQLMQVLDEAHKQRKTGRFLFLTLTAENASGENLKQEVRKMGR 128
                                            AWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNG-WHVHVHALLMFSGDVSENILESFS 190
                                                                          191 DAMFDRWISKLVSLGFAAPLRNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGK 250
                                                                                                                                                                                            226
                                                                                                                                                                                                                        251 SGRHGNRAPWEI-AVDAVGGDPQA-LELWREFEFGSMGRRAIAWSRGL--RARAGLGAEL 306
                                                                                                                                                                                                                                                 58 IVNGPKGSGFGGLR----SCGKGWICPCCAGKVGAHRADEISQVV---AHQLGTGSVAM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 VIMIMRHTAGQRLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGKNG--W 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KKQGEILVDKNSRGKERDWRGRKILSLKLADIFKELQYKKTFVERVISCGDTLQFIQNQD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication protein repA - Streptococcus thermophilus
C;Species: Streptococcus thermophilus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                12 KORPPVLVSSDKRGIRHELRP-----KLQQI-----TTSBTFNACGRPISGVNGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A,Molecule type: DNA
A,Residues: 1-315 <SGL.
A,Cross-references: UNIPROT:Q9RNW4; EMBL:AF177167; PIDN:AAF04355.1
A,Experimental source: strain ST135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 123.5; DB 2; Length (2.8%; Pred. No. 0.016; Ve 41; Mismatches 79; Indels
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                                                                                                                                                                                                                                                                                                              307 TDAQIVEQEE 316
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279 VDAHLINVDD 288
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Local 50; Conserva
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A; Genome: plasmid
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A;Title: A small plasmid, pCA2.4, from the cyanobacterium Synechocystis sp. strain PCC 6
A;Reference number: A40651; MUID:93308076; PMID:8320214
A;Accession: A40651
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 < YAN>
A;Coss-references: UNIPROT:Q06460; GB:L13739; NID:G408891; PIDN:AAA02970.1; PID:G290013
A;Genome: plasmid
C;Superfamily: replication protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 MRHTAGORLHDLWTGLSAAWKAATNGRRWRTEREMYGCDGYVRAVEITHGK--NGWHVHV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 VKNIEGKALNSTISQLTKSFDRLF--KRAKVQRNLL---GYLRSVEVTHNENDNSYHPHI 172
                                                                                                                                                                                                                                                79 CPCCAGK---VGAHRADEISQVVAHQLGTGSVAMVTMTMRHTAGQRLHDLWTGLSAAWKA 135
                                                                                                                                                                                                                                                                      97 CPVCQWRRSLMWRAKAFKILDQIVBAYPKHRFIFLTLTVRNCELGQLRETITGMNQAMGR 156
                                                                                                                                                                                                                                                                                                             136 ATNGRRWRIEREMYGCDGYVRAVEITHGKNG-WHVHVHAHLLM----FS-GDVSENILES 188
                                                                                                                                                                                                                                                                                                                             LVKRAKW-----PADGWIRSLEVIRGKDGSAHPHFHCLLMVKASYFSHGYISQEV--- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --TISETFNACGRPISGVNGVTIVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 NGKDR------DWRG-RKILSLKLADIFKELQYKKTFVERVISCGDTLRFIQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 314;
                                                                                                                                                                                    ch 5.7%; Score 115; DB 2; Length 336; 1 Similarity 26.2%; Pred. No. 0.083; 34; Conservative 23; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 25.4%; Score 114; DB 2; Similarity 25.4%; Pred. No. 0.093; 17; Conservative 33; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: rep
A;Genome: plasmid pER341
C;Superfamily: replication protein
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                                                                                                                                                                                                                                                                                                                                                                              189 FSDAMFDRWT 198
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HVLMM 177
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Best Local Similarity
Matches 34; Conserv
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Best Local S
Matches 47
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replication initiation protein rep [similarity] - Bacillus subtilis plasmids
N.Contains: DNA ligase (EC 6.5.1.-); DNA lyase (EC 4.2.99.-)
C;Species: Bacillus subtilis
C;Species: DoMar-1994 #text_change 09-Jul-2004
C;Accession: A49783; S70201
R;Hara, T.; Nagatomo, S.; Ogata, S.; Ueda, S.
R;Hara, T.; Nagatomo, S.; Ogata, S.; Ueda, S.
A;Title: Molecular structure of the replication origin of a Bacillus subtilis (natto) p
A;Title: Molecular structure of the replication origin of a Bacillus subtilis (natto) p
A;Reference number: A49783; MUID:9136725; PMID:1840479
A;Residues: 1-33 cHAR>
A;Accession: A49783
A;Molecula type: DNA
A;Residues: 1-33 cHAR>
A;Residues: 1-33 cHAR>
A;Residues: 1-33 cHAR>
A;Residues: 1-34 cHAR>
A;Residues: 1-35 cHAR>
A;Experimental source: strain natto, plasmid pUH1
A;Note: authors translated the codon CCA for residue 45 as Ala, and GCA for residue 142
A;Note: authors translated the codon CCA for residue 45 as Ala, and GCA for residue 142
A;Note: authors translated be codon CCA for residue 45 as Ala, and GCA for residue 142
A;Note: authors translated be codon CCA for plasmid pUH1
A;Note: authors translated be codon CCA for plasmid pUH1
A;Note: authors translated be codon CCA for plasmid pUH1
A;Note: authors translated be codon CCA for plasmid pUH1
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Sisteman, S.D.; Warrener, P.; Hickey, M.J.; Assistance, C., Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Assistance, C.Y.; Phan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li.; Lory, S.; Olson, M.V.

Nature 406, 955-964, 2000
A;Tille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1:381 <STO>
A;Cross-references: UNIPROT:Q915P2; GB:AE004503; GB:AE004091; NID:g9946553; PIDN:AAG04
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0683
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Ajactession: 870201
Ajactus: mucleic acid sequence not shown; translation not shown
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule type: DNA
Ajmolecule the nucleotide sequence was submitted to the EMBL Data Library, August 1994
CjGenetics:
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C.Keywords: carbon-oxygen lyase; ligase; plasmid replication
C;Keywords: carbon-oxygen lyase; ligase; plasmid replication
F;245/Active site: Tyr (covalent DNA-binding) #status predicted
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Pred. No. 0.63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%;
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Best Local Similarity

RESULT 11 A49783 Ŋ

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heme biosynthesis protein [imported] - Nostoc sp. (strain PCC 7120)
Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. ptc 7120
A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
E;Kaneko, T.; Nakamura, Y.; Wollk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1.420 <KUR>
A;Cross-references: UNIPROT:Q8YVE9; GB:BA000019; PIDN:BAB73728.1; PID:g17131120; GSPDB
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2029
                                                                                                        135 AATNGRRWRIEREMYGCDGYVRAVEIT--HGKNGWHVHVHALL-MFSGDVSENILESFSD 191
                                                                                                                                                146 KLFQYKKVKT----SVLGFFRALEITKNHEEDTYHPHFHVLIPVRKNYFGKNYIKQ--- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 KVGAHRADEISQVVAHQLGTGSVAMVIMIMRHIAG-QRLHDLWIGLSAAWKAAINGRRWR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 APWEIAVDAVGGDPQALELWREFEFG--SMGRRAIAWSRG---LRARAGLGAELTD---A 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 -PYE---RLLRGQGKEWGFWRGCGAGLSTLGLEADGTIKGCPSLPTTAYAGGNIRERPLR 288
                  GYG-----ISLEMAQRMKEAGIAKVSVS---TDGMEATHDHLRGRKGSWKSGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 QELSTAEALNLVQQLAEVGIKEVTLIGGE----AFLRPDWLVIAKAITDAGMLCGMTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEREMYGCDGYVRAVEITHGKNGWHVHVHAHALLMFSGDVSENILESFSDAMFDRWTSKL-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLGFAAP-----LRNSGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 PMGNAADNADILLOPSELLDL-----YPMLARVAORANTEGVRVAAGN-NIGYYG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 104; DB 2; Length 420; 24.4%; Pred. No. 0.86; Live 47; Mismatches 135; Indels
                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 QQITTSETFNACGRPIS-GVNGVTIVNGPKGSGFGGLRS
                                                                                                                                                                                                                                                              ---AEWTSLWKKAMKLDY-TPI----VDIRRVKGKA
                                                                                                                                                                                                                               AMFDRWTS---KLVSLGFAAPLRNSGGLDVRKIGGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 24.49
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application initiation protein rep60 [validated] - Bacillus subtilis plasmids NoContains: DNA ligase [EC 6.5.1.-); DNA lyase [EC 4.2.99.-)

NoContains: DNA ligase [EC 6.5.1.-); DNA lyase [EC 4.2.99.-)

C;Deccession: 140561; A32059; A340997; 140549

R;Maijer, N.J.; Venema, G.; Bron, S.

NuCleic Acids Rese. 23, 62-619, 1995

A;Title: Characterization of single strand origins of cryptic rolling-circle plasmids francesion: 140549; MUID:95206941; PMID:7899081

A;Reference number: 140549; MUID:95206941; PMID:7899081

A;Reference number: 140549; MUID:95206941; PMID:7899081

A;Reference rightmary; translated from GB/EMBL/DDBJ

A;Reference plasmid pTAA.06

B;Reference number: 1340 -MEI:

A;Reference number: 1340 -MEI:

A;Reference number: 1340 -MEI:

A;Reference number: 1340-MEI:

A;Reference number: 1340-MEI:

A;Reference number: 1340-MEI:

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A;Reference number: 1340-MEI:

A;Reference number: 134
                                                       WICPCCAGKVGAH--RADEISQVVAHQLGTGSVAMVTMTMRHTAGQRLHDLWTGLSAAWK 134
                                                                                                                                                                     135 AAINGR------VWRIEREMYGCDGYVRAVEITHGKNGWH------VHVHALL 175
                                                                                                                             -- OELRLFWLGERPAWR 174
                                                                                                                                                                                                                               175 SAALERAEALDEALRWSGPASPWGL--ALKAPATSAGNGTWRWPLFCAALALLVWVAGLN 232
                                                                                                                                                                                                                                                                                                      -PLRNSGGLDVRKIGGEADOVL 229
                                                                                                                                                                                                                                                                                                                                                 233 LYAGOLAE-----QGOSLOROSSORVOQAFPELPVVLDPLRQARERRDAYLAGKADGDA 286
                                                                                                                                                                                                                                                                                                                                                                                                        230 AAYLIKIASGVGMEVGSGDGKSGR---HGNRAPWEIAVDAVGGDPQALBLMREFEFGSMG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGLAALLHGAGEAMPFLAGRLQRLDYHAGELDLELLPGLPGGDAAA---W-QGELGKHG 342
               Gaps
            54;
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         Indels
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                                                                                                              127 WV----AGEWDGHLLLRRSLSDAVVHPLPEQGLAEVP---
   Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                                                          176 MFSGDVSENILESFSDAMFDRWTSKLVSLGFAA----
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C;Superfamily: replication protein
C;Keywords: carbon-oxygen lyase; li
F;25/Active site: Tvr (covalent na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| | :| : ||
343 LQADASDKGWQVRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 RRAIAWSRGLRARA 300
   Conservative
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Best Local Similarity 24.2%
Warches 38; Conservative
90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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23;

Gaps

82;

84

257 232

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D-amino-acid dehydrogenase (EC 1.4.99.1) [imported] - Brucella melitensis (strain 16M) c;Species: Brucella melitensis () Species: Brucella melitensis () Species: Ol-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004 () Accession: AC3284 () Repatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Moltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Tile: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                         331
310 QIVEQEESAPV-MVAIIP---ARSWMMIRTCAPYVFGEILGLVEAGATW 354
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78 ICPCCAGKVG---AHRADEISQVVAHQLGTGSVAMVTMTMRHTAGQRLHDLWTGLSAAWK 134

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A;Accession: AC3284
A;Status: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Coss-references: UNIPROT:Q8YJ30; GB:AE008917; PIDN:AAL51438.1; PID:g17982146; GSPDB:G
A;Coss-references: UNIPROT:Q8YJ30; GB:AE008917; PIDN:AAL51438.1; PID:g17982146; GSPDB:G
G;Genetics:
A;Gene: BME10256
A;Gene: BME10256
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                        153 GYVRAVEITHGKNGWHVHVHALLMFSGDVSENILESFSDAMFDRWTSKLVSLGFAAPLRN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 SGGLDVRKIGGEADQVLAAYLTKIASGVGMEVGSGDGKSGRHGNRAPWEIAVDAVGGDPQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ALELWREFEFGSMGRRAIAWSRGLRARAGL---GAEL----TDAQIVE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 RGYNTTLPVGSFDVKRQLTFPGHGFVITPMETGLRVGGAVEFGGLDLPPNFARSEAMLKK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 QEESAPVMVAIIPARSWMMIRTCAP------YVFGE-ILGLVEAGATWEN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 SQVVAHQLGTGSVAMVTMTMRHTAGORLHDLWTGLSAAWKAATNGRRWR--TEREMYGCD 152
                                                                                                                                                                                                                                                                                                                                       209 ------GKAIW------SYAESLGARFLSGKV----ASAKRQ 234
                                                                                                                                                                                                                                                                         93; Gaps
                                                                                                                                                                                                                                    Length 420;
                                                                                                                                                                                                                                Query Match
5.1%; Score 102.5; DB 2; Length 4
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 63; Conservative 49; Mismatches 111; Indels
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Job time : 26 secs
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UI-M-FWO-UI-M-FDO-

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number

Searched:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 929)

2 NIH-MGC http://mgc.nci.nih.gov/.

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Uppublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Dr. David Rowe

6 DNA Library Preparation: Invitrogen Corp

6 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 DNA Sequencian by: Agencourt Bioscience Corporation

6 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 COND clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8 Plate: LLAM14097 row: g column: 03

8 High quality sequence start: 6

8 High quality sequence start: 6

8 High quality sequence start: 6

9 Town of the column: 03

10 Contact the column: 03

11 Docation/Qualifiers
                                                                                                                                                                                                                                                                                    EY1738T BY717387
AK049163 MUS muscu
AK08202B MUS muscu
BC013842 MUS muscu
BC013842 MUS muscu
BX077609 MUS muscu
BY729572 BY729572
BZ551248 pacs1-60
CL829504 CR CBa005
BG922360 602820270
                                                                            BX898881 BQ936859 PBF783863 6
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BI411296
CA280312
BG684181
CB248284
BQ572893
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CA750314 1
BY717387 1
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BQ672428 P
CL495997 S
BQ276790 A
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CF724491
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                                                              BZ554247
                                  BI224374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BUS19534 929 bp mRNA linear EST
AGENCOURT 10166703 NIH MGC 134 Mus musculus cDNA clone
IMAGE:6517370 5', mRNA sequence.
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 BU271357
BM907785
BI224374
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BU705875
CF734491
CF724491
CF734522
BI41129
CA23522833
BG684181
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AK049163
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AK083015
BC013842
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CL495997
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Mus musculus
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BM47396 AGENCOURT
AG347460 Mus muscu
BI661991 601304986
AY411933 HOMO SADI
CC653500 OCVEQ46TM
CC623500 OCVEQ46TM
CC479652 SAIL 30 C
CC321442 TAM32-34D
                                                                                      October 23, 2004, 04:02:18; Search time 3866 Seconds (without alignments) 3572.338 Million cell updates/sec
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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EST 12-SEP-2002

Database :

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1 (bases 1 to 1648)

Nath-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                             330 TrpMetMet1leArgThrCysAlaProTyrValPheGlyGlulleLeuGlyLeuValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 AlaGlyAlaThrTrp-GluAsnLeuArgAspHisLeuHisTyrArgLeuProAlaAlaAs
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llnl.gov
http://image.llnl.gov g column: 07
High quality sequence stop: 263.
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Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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and Chemical Research (RIERN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-mail:hattorieges.rikken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyada, Tsukuba 135-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                              2 (bases 1 to 2033)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
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                                                    Mus musculus molossinus
Mus musculus molossinus
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                  Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/mol_type="genomic DNA"
/sub_species="molossinus"
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AG347460/c 2033 bp DNA linear GSS 02-JUN-2004
LOCUS AG347460
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-142P21.TJ, genomic survey
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KEYWORDS EST. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus URGANISM musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 894) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Context: Robert Strausberg, Ph.D. Email: cgapba-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth	Ph.D. DNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI1891 row: k column: 22 High quality sequence stop: 849. Location/Qualifiers 1. 894 /organism="Mus musculus" //organism="Mus musculus" //organism="Mus musculus" //db_xref="taxon:10090" /clone="INAGE:357097" /tissue_type="tumort, gross tissue"	/dev stage="S months" /lab host="DH10B" /lab host="DH10B" /rote="Corgan: mammary; Vector: pc Site 2: Not1; Cloned unidirection Library constructed by Life Techn providing samples: Lothar Hennigh NIH Reference for transgenic mode and Differentiation 7, 3-11 (199	Pred. No.: 0.276 Length: 894 Score: 122.50 Matches: 79 Percent Similarity: 30.77% Conservative: 25 Best Local Similarity: 23.37% Mismatches: 114 Query Match: 6.11% Indels: 120 DB: 4 Gaps: 16 US-10-007-527A-2 (1-379) x B1661991 (1-894)	68 GlyGlyLeuArgSerCysGlyLysGlyTrpIleCysPro 8	Cy CysCysAlaGlyLysValGlyAlaHisArgAlalleSer 95	Qy 116 HisThrAlaGlyGlnArgLeuHisAspLeuTrpThrGlyLeuSer 130	Oy 131 AlaAlaTrpLysAla
1716 GGAGTCGGGTGGTTGAGTGAGGTGGTGGCTGCTTGCGTGTGCGCGGCTGGCGGGGGTGT 87 G1yAla	Date Using the Control of Con	Qy 161 ThrHisGlyLysAsnGlyTrpHisValHisValHisAlaLeuLeuNet	Qy 200 LysLeuValSerLeuGlyPheAlaAlaProLeuArgAsnSerGlyGlyLeu 216		CY 250 DysselctyArgansbrandarjariarioirporulieAlavaasbrandarjay 269	QY 290 IlealaTrpSerArgGlyLeuArgAlaArgAlaArgAlaArg1yLeuGly 303	RESULT 5 BI661991/C LOCUS BI661991/C LOCUS BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991 BI661991

Rockville, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers 12887 /mol_type="genomic DNA" /db_xref="texon:9606" 21>2887 /locus_tag="HCM4389"	Scores: 1.57 122.00 imilarity: 33.61 1 Similarity: 23.14 ch: 9.08	-10-007-527A-2 (1-379) x AY411933 (1-2887) 17 ValLeuValSerSerAspLysArgGly1leArgHisGluLeuArgProLysLeuGlnGln 36 17 ValLeuValSerSerAspLysArgGly1leArgHisGluLeuArgProLysLeuGlnGln 36 1440 GTCCTGCTGGCTGGACCAGGACATGCCATCCTCCTGGGCCTGTGGCAGCGGCGTGGGCGG 13 37 IleThrThrSerGluThrPheAsnAlaCysGlyArgProlleSerGlyValAsnGlyVal 56 :::	Db 1380 CTGGCTGCAGCTCAGGTCCTCCATGGTGCTGTAGTCTCCGGACTTGACGCCCAG 1321 Qy	1261 TGGGGGGTACTTGTGCGGGGGGGGGGGGGGGGGGGGGGG	Oy 134 sAlaAlaThrAsnGlyArgArgTrpArgThrGluArgGluMetTyrGlyCysAspGlyTy 154 Oy 134 sAlaAlaThrAsnGlyArgArgTrpArgThrGluArgGluMetTyrGlyCysAspGlyTy 154 Db 1081 TGTTGGGCTGGAGGAGGCCGGGGCTTACGGCCGGGGACCGGCGTT 1022 Oy 154 rvalArgAlaValGluIleThrHisGlyLysAsnGlyTrpHisValHisValHisAlaLe 174 155	982 GCTCATCGTAGATGGG	Db 919 919 Qy 234 rLysIleAlaSerGlyValGlyWetGluValGlySerGlyAspGlyLysSerGlyArgHi 254
LysAsnGlyTrpHisValHisValHisAlaLeuLeuMetPheSerGlyAspValSerGlu	224 GlualaAspGlnValLeuAlaAlaTyrLeuThrLysIleAlaSerGlyValGlyWet 242 224 GlualaAspGlnValLeuAlaAlaTyrLeuThrLysIleAlaSerGlyValGlyWet 242 403GGAGGATCCTCTGAGGGGATCTTGCCGATTGACCAACATAAACAGTTGT 350 243 GluValGlySerGlyAspGlyLysSerGlyArgHisGlyAsnArgAlaProTrpGluIle 262 349 ACTCTTTGTTGGTGGGGGAATGGGGAAACGGGGGAGCCAGGGTCAGGTGGGGCT 290	263 AlavalAspAlaValGlyGlyAspProGlnAlaLeuGluLeuTrpArgGluPheGluPhe 282	303 GlyAlaGluLeuThrAspAlaGlnIleValGluGlnGluSerAlaProValMetVal 322	GlulleLeuGlyLeuValGluAlaGlyAlaThrTrp-GluAsnLeuArgAspHisLeuHi	3/C AY411933 2887 bp DNA linear GSS 12-DEC-2003 TON Homo sapiens HCM4389 gene, VIRTUAL TRANSCRIPT, partial sequence, ON AY411933 AX411933.1 GI:39767898 S GSS Homo sapiens (human) Homo sapiens (human)	Euka: Mamma 1 (1) Clar Todd Ferr: Adam:	gene trios Grence 302 (5652), 1960-1963 (2003) BD 14671302 C (bases 1 to 2887) CC 2 (bases 1 to 2887) RS Clark, A.G. (Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission S Direct Submission S Lower Gude Drive,
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Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1255)
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1 (Dases 1 to 918)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGYEQ46TC
Contact: Cathy Whitelaw
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/clone="xx/mBMa6501G19"
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/mol_type="genomic DNA"
/strain="B73"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 1661)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Gallus gallus BAC End Reads
Unpublished (2003)
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                                                                                                                                                                                                                                                                                         3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com
ABRC Stock Number CS801460, T-DNA left border flanking sequences o
Syngenta Arabidopsis Insertion Library (SAII) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Single contiguous sequences.
Class: TDNA tagged.
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Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mizel, T., Katagiri, F., Glazebrock, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
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was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., pNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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1 (bases 1 to 950)
Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Cuprehensive Collection of Chicken cDNAs
Cuprehensive Collection of Chicken cDNAs
22335534
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                          --GluvalGlySerGlyAspGlyLysSerGlyArgHisGlyAsnArgA
                                                                  .------ArgGluPheGluPheGlyS
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Department of Blomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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		AUTHOR IN LABORS IN LOTATORY AUTHORY TITLE National Institutes of Health, Mammalian Gene Collection (MGC) TORNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTD/Gazdar CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://imag-llnl.gov Plate: LLAM12744 row: f column: 10 High quality sequence stop: 319.	Source 11430 Jorganism="Homo sapiens"	Alignment Scores:
Igin ignment Scores: 0.657 Length: 950 ore: 119.00 Matches: 80 ore: 139.00 Matches: 31 st Local Similarity: 21.68\$ Conservative: 31 st Local Similarity: 21.68\$ Mismatches: 120 ery Match: 5.94\$ Indels: 139 caps: 17 -10-007-527A-2 (1-379) x BU271357 (1-950) ery Match: 1379 x BU271357 (1-950) ery Match: 1379 x BU271357 (1-950) ery Match: 1379 x BU271357 (1-950)	Db 909 TATGGTCTTTGCCGGGGTGTTGTTGGGGGGGGGGGGGGG	117 raladlyGlnArgLeuHisAspLeuTrpThrGlyLeuSerAlaAlaTrp-LysAlaAlaTry raladlyGlnArgLeuHisAspLeuTrpThrGlyLeuSerAlaAlaTry-LysAlaAlaTry raladlyGlnArgGlyTrGGTTTGGTTTGGTTTGGCGTGGG range ra	187 LuSerPheseraspalametPheaspargTrpThrSerLysLeuValSerLeuGlyPhea 207 187 LuSerPheseraspalametPheaspargTrpThrSerLysLeuValSerLeuGlyPhea 207 187 LuSerPheseraspalametPheaspargTrpThrSerLysLeuValSerLeuGlyPhea 207 187 LuSerPheseraspalametPheaspargTrpThrSerLysLeuGlyPhea 207 187 LuSerCheuValgasnSerGlyGlyLeuAspVallargLyslleGlyGludlaAspG 227 Db	429 GGTGGAGCAGGGTGTGA

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 1687)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

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770 TAGCGGAATCAGGCGGCTGTAATGAGTCCATAAGGGTGTGCCGANAAGTCCATGAGTGTG
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|064 GACTATCGCT---AAACAT----
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-ValGlyAlaHisArg

---AGGGGGTGGCGA-- 781

EST 11-JUL-2001

linear

mRNA

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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6307476"
/lab host="DH10B (phage-resistant)"
/clone="Organ: olfactory epithelium, Vector: pCMV-SPORT6.1;
Site_1: ECGRV; Site_2: NotI; Cloned unidirectionally.
Primer: oligo dT. Average insert size 2: 2kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
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Mismatches:
Indels:
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Matches:
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Query Match:
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5', mRNA Sequence.
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lHisValHisAlaLeuLeuMetPheSerGlyAspValSerGluAsnIleLeuGluSerPh 189
                                                                                                                                                                                                                                                                                                                          -----GAGAGCGCGCGCGCGCTGTGAGCAGGCAGCCCCTGGGGAGAA 599
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NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: Resden, Invitrogen Corp
cDNA Library Arrayed by: The I M.A.G.E. Consortium
CLONA Library Arrayed by: The I M.A.G.E. Consortium
CLONA Gistribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 666.
Location/Qualifiers
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                                                                       eSerAspAlaMetPheAspArgTrpThrSerLysLeuValSerLeuGlyPheAlaAlaPr
                                                                                                                                                                                                                                        aAlaTyrLeuThrLysIleAlaSerGlyValGlyMetGluValGlySer------
                                                                                                                                                                                                                                                                                                                                                            ----GlyAspGlyLysSerGlyArgHisGlyAsnArgAlaProTrpGluIleAlaValAs
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                                                                                                          ------GGCAACAGCGCGCC
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Qy 51 SerGlyValAsnGlyValThrIleValAsnGlyProLysGlySerGlyPheGlyGlyLeu 70 bb 611 GTTGGC		Db 363 CCGGGGGGGGGCCTGTTCCGGTAGTCGGGGCGAGGTTGGCA Qy 170 HisValHisAlaLeuLeuMctPheSerGlyAspValSerGluAsnIleLeuGluSerPhe 189 Db 309	Qy 208AlaProLeuArgAsnSerGlyGlyLeuAspValArgLysIleGly 222	0 7 0	BX898881 Oryza sativa library (Han B) Oryza sativa CDNA y828f11p5, mRNA sequence. BX898881. GI:40488387 EST. Oryza sativa Oryza sativa Evaryota; Viridiplantae; Streptophyta; Embryophyta; Trasspermatophyta; Magnoliophyta; Liliopsida; Poales; Poace:	n n n n n n n n n n n n n n n n n n n
Db 317 GCTGGGCTCAGCTGGGCTCAGGCAGAGAACTGGGGCAGGA	Db 221 Gractcccddgracgccagacacagacacagacacacacacacacacaca	ACCESSION BZ554247 VERSION BZ554247 VERSION BZ554247 VERSION BZ554247.1 KEYWORDS GSS. SOURCE Pseudomonas aeruginosa ORGANISM Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. REFERENCE I (bases I to 893) AITHRORS Spencer D.H. Raymond.C.K., Smith.E.E., Sims.E.E., Hastings.M.,	Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol. (2002) In press Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA	uginosa"	/note="clinical is library." [GIN library." GAN O.: 0.754 Dre: 0.754 Dre: 34.07 Fre Local Similarity: 27.118 ery Match: 5.89\$	Gaps: 1-893

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Clone requests: bhandangr.ac.cn
This is rice cdna est clone
Web site: http://www.nogr.ac.cn.
Location/Qualifiers
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500# Cao Bao Road, Shanghai 200233, China
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